

GenCore version 5.1.4-p5\_4578  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: May 7, 2003, 15:14:59 ; Search time 200 Seconds

(without alignments)  
6700.652 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257

Perfect score: 6089

Sequence: 1 atgcgcgcacatgcggggcct.....aagaagcacacaggggtctga 3252

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=SPTRMBL_21 -QMT=fastan -SOFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human4.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=DCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09965830 @CGCN.1.1.350 @runat_07052003_151449_6257 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEROUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2	5428	89.1	1087	11	089047	089047	rattus norv
3	5416	88.9	1087	11	09WV0	09WV0	mus musculu
4	2529.5	41.5	1107	4	096L42	096L42	homo sapien
5	2515	41.3	1102	11	088877	088877	rattus norv
6	2461.5	40.4	1017	4	09U005	09U005	homo sapien
7	2447.5	40.2	1017	11	09R179	09R179	rattus norv
8	2439.5	40.1	1017	11	089048	089048	rattus norv
9	1901	31.2	1284	5	023974	023974	dracophila
10	1901	31.2	1311	5	09W899	09W899	canis famli
11	1551	25.5	1158	6	09T823	09T823	mus musculu
12	1547	25.4	1162	11	035221	035221	mus musculu
13	1543	25.3	1162	11	08WNT2	08WNT2	mus musculu
14	1539	25.3	1162	11	035219	035219	mus musculu
15	1537.5	25.3	1163	11	008962	008962	rattus norv
16	1509.5	24.8	994	4	09H282	09H282	homo sapien
17	1499.5	24.6	1144	6	019119	019119	oryctolagus
18	1475	24.2	950	11	054853	054853	rattus norv
19	1400.5	23.0	1195	11	09ER47	09ER47	mus musculu
20	1395.5	22.9	1195	11	054852	054852	rattus norv
21	1387	22.8	1174	5	09VX26	09VX26	dracophila
22	1384.5	22.7	1196	4	09N540	09N540	homo sapien
23	1380.5	22.7	962	11	063472	063472	rattus norv
24	1378	22.6	960	6	018965	018965	bos taurus
25	1371.5	22.5	989	11	060603	060603	mus musculu
26	1369	22.5	962	4	076035	076035	bos taurus
27	1367.5	22.5	987	6	018966	018966	bos taurus
28	1361	22.4	888	4	09H3P0	09H3P0	homo sapien
29	1358.5	22.3	989	4	095259	095259	homo sapien
30	1339.5	22.0	988	11	09QXT2	09QXT2	rattus norv
31	1337.5	22.0	988	11	09EP19	09EP19	homo sapien
32	1268.5	20.8	820	11	035989	035989	rattus norv
33	1261.5	20.7	956	5	09XXY7	09XXY7	mus musculu
34	1259.5	20.7	956	5	044164	044164	caenorhabdi
35	1257.5	20.7	820	11	035220	035220	mus musculu
36	1232	20.2	366	11	09QWS8	09QWS8	rattus norv
37	1185.5	19.5	772	4	09BUT7	09BUT7	homo sapien
38	1084	17.8	791	5	018325	018325	caenorhabdi
39	1046	17.2	855	5	002497	002497	dracophila
40	1035.5	17.0	526	13	09PT84	09PT84	gallus gall
41	938.5	15.4	502	4	09HBD7	09HBD7	homo sapien
42	577	9.5	1198	11	09JKA7	09JKA7	rattus norv
43	566	9.3	1203	4	09UM07	09UM07	homo sapien
44	562.5	9.2	1175	6	09TV66	09TV66	oryctolagus

## ALIGNMENTS

## RESULT 1

Q9ULD8 PRELIMINARY; PRT; 1117 AA.

AC Q9ULD8; Q9U006; 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DE 01-UN-2002 (TREMblrel. 21, Last annotation update)

GN KIAI1282 protein (BEC1) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_Taxid:9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE-20039619; PubMed-10574462;

RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.,

RT The complete sequences of the coding sequences of unidentified human genes. XY.

RT for large proteins in vitro.,"

RL DNA Res. 6:337-345(1999).

RN [2]

RP SEQUENCE OF 35-1117 FROM N.A.

RC TISSUE-BRAIN;

FX	MEDLINE=99386988; Pubmed=10455180;	
RA	Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuchi K.,	
RT	"New ether-a-go-go K <sup>+</sup> channel family members localized in human	
RT	telencephalon."	
RL	J. Biol. Chem. 274:25018-25025(1999).	
DR	EMBL; AB033108; BAA86596.1; "-	
DR	EMBL; AB022696; BAA83590.1; "-	
DR	InterPro: IPR000595; CNMP_binding.	
DR	InterPro: IPR001622; K-channel_pore.	
DR	InterPro: IPR000636; M-channel_10.	
DR	InterPro: IPR001610; PAC.	
DR	InterPro: IPR000700; PAS-assoc_C.	
DR	InterPro: IPR000014; PAS_domain.	
DR	Pfam; PF00027; CNMP_binding; 1.	
DR	Pfam; PF00520; Ion_trans; 1.	
DR	Pfam; PF00785; PAC; 1.	
DR	SMART; SM00100; CNMP; 1.	
DR	SMART; SM00086; PAC; 1.	
DR	SMART; SM00091; PAS; 1.	
DR	TIGRFAMs; TIGR00229; sensory_box; 1.	
DR	PROSITE; PS00042; CNMP_BINDING_3; 1.	
FT	NON_TER	
SQ	SEQUENCE	
	1117 AA; 120471 MW; 163k100B/7141cA53 CRC64;	

Alignment Scores:	
Pred. No.:	5, 12e-309
Score:	5704, 00
Percent Similarity:	100, 00%
Best Local Similarity:	100, 00%
Query Match:	93, 68%
DB:	4
US-09-965-830-1.COPY_6_3257 (1-3252) × Q0ULD8 (1-1117)	
	Length: 1117
	Matches: 1080
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

OY	1	ATGCCGCATCGGGGCTCTCGCGCCCTCAGAACACCTTCTGGACACCAATCGCTAGG	60
Db	35	MetProAlaMetArgIleuLeuAlaProGlnAsnThrPheLeuSphTrIleAlaThr	54
OY	61	CGCTTCAGCGGACGACGACAGAAATTCGTGCTGGGCAACGCCAGAGTGGCGGGCTCTTC	120
Db	55	ArgPheAspGlyThrHisIleSerAsnPheValLeuGlyAsnAlaIleValIleGlyLeuPhe	74
OY	121	CCCGGAGCTACTGCTGATGAGCTTGTGACTCCAGCGGCTTCTCCGGGCTGAGGTC	180
Db	75	ProValValIleTyrCysSerAspGlyPheCysAspLeuThrClyPheSerArgAlaGlyVal	94
OY	181	ATGCAGCGGGGCTGTGCTCTCTCTCTCTCTCTTATGGGCCACAGATGAGCTGTCTGGC	240
Db	95	MetGlnArgGlyCysAlaCysSerPheLeuTyrClyProAspThrSerGluLeuValArg	114
OY	241	CAACAGATCCGACAGGCCCTGACAGACACAGAGATTCAAGGCTGAGCTGATCCGTGAC	300
Db	115	GlnGlnIleArgIysAlaIleuAspClyHisIleGlyLeuPheGlyAsnGlyLeuIleTyr	134
OY	301	CGGAAAGCGGGCTCCCTGTTCTGTGTCTCTGGATGATGATACCATAAAGATGAGAAA	360
Db	135	ArgIysSerGlyLeuProPheThrPtyLeuLeuAspValIleProIleIysAsnGluIys	154
OY	361	GGGAGAGTGGCTCTCTCTTAATCTCTACAAAGACATCAGCGAACAACGAGCGAGG	420
Db	155	GlyGlyValAlaIleuPheLeuValSerHisIlyAspIleSerGlyThrThrIysAsnArgGly	174
OY	421	GGCCCCGACAGATGGAAGAGACAGAGTGGCGGGCCGATATGGCCGGGACAGATCC	480
Db	175	GlyProAspArgTyrPtySerGlyThrThrIleGlyGlyArgAlaGlyTyrGlyArgAlaArgSer	194
OY	481	AAGGCTTCAATGGCCAAACCGGGGCGGAGACCGGCGCTGTCTACCACTTGTCCGGGAC	540
Db	195	LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValIleuTyrHisIleuSerGlyHis	214
OY	541	CTGACAGACGACCCAAAGGCAAGACACAAAGTCAATTAAGGGGGGTGTTGGGAGAAAACA	600
Db	215	LeuGlnIysGlnProIySerGlyIysHisIysIysLeuAsnIysGlyValPheGlyGlyIysPro	234

OY	601	AACCTGCGTAGTACAAGATGACGCCGCATTCCGGAAAGTCGCCCTCATCCTGTTCACAGT	660
Dd	235	AsnLeuProGluTyrLysValAlaAlaIleThrGlySerProPheIleLeuLeuHisCys	254
OY	661	GCGGCACTGAGAGCCACTGGGATGGCTTCATCCCTGCTGGCACACTGTATGGCTGTC	720
Dd	255	GlyAlaLeuAlaGlaIleThrTrpAspDylPheIleLeuLeuAlaIleThrLeuTyrValAlaVal	274
OY	721	ACTGTGCCCTACAGCGTGTTGTGTGAGCACACAGCAGGGAGCCAGTGCCTGGCCGGCCG	780
Dd	275	ThrValProTyrSerValCysValSerThrAlaArgLuproSerAlaAlaArgLupro	294
OY	781	CCCAGCGTGTGAGCTGGCCCTGGAGAGCCCTCATCCCTTGACATTTGGTGAATTC	840
Dd	295	ProserValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	314
OY	841	CGRACCAATGGTGTCCAAAGTCGGGGCAGTGGTGGTGGCCCAAAGTCATTTGCTC	900
Dd	315	ArgThrThrPheAlaSerTyrSerGlnValValAlaPheAlaProLysSerIleCysLeu	334
OY	901	CACATAGCTACACACTGTCTCTGATGATGCATGCAGCGCTGCCCTTTGACCTGTA	960
Dd	335	HistYrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	354
OY	961	CATGCGCTCAAGGTCAACSTGTACTTCTGGGGCCCCAATCCTGTGAAGAAGGTGGCCMGCG	1020
Dd	355	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	374
OY	1021	CGGCTGTGGCGCTGGTCCGGCGGCGGAGACCCTGACTCCAGTACAGCCCGCTGGCTG	1080
Dd	375	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValAlaLeu	394
OY	1081	ACACTGCTCATGGCCGCTGTTCGCGCTGCTGGCGACTGGGTGGCTGCTGCTTTAC	1140
Dd	395	ThrLeuLeuMetAlaValAlaPheAlaLeuLeuAlaHisTyrValAlaCysValTrpPheTyr	414
OY	1141	ATTGGCCAGCGGGAGATCGAGACAGACAGGATCCGAGTCCGAGTGGCTGGCTGGAC	1200
Dd	415	IleGlyGlnArgGluIleGlnSerSerGlnSerGluLeuProLueIleGlyTrpLeuGln	434
OY	1201	GAGTGGCCGCGCAGTGCAGACCTCCTACTACTGGTGGCGCGGAGCCAGCTGAGGG	1260
Dd	435	GluLeuAlaArgArgLeuGlnThrProTyrTyrLeuValGlyArgProAlaGlyGly	454
OY	1261	AACAGCTCCGGCCAGAGTGACACTGCAGACAGCAGCAGGACGAGGAGGGGCTG	1320
Dd	455	AsnSerSerGlyGlnSerAspAsnCysSerSerSerGlnAlaAsnGlyThrGlyLeu	474
OY	1321	GAGCTGCTGGGCGGCCGCTGCTGCTGGCAGCGCCATCAACCTCCCTTCCTTGGCACTC	1380
Dd	475	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	494
OY	1381	AGCAGCCACACAGGATGGGTTCGGGCAACTGTCCGCCAACAGCAGCAGCCAGAGATC	1440
Dd	495	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluTyrIle	514
OY	1441	TTCCTCATCTGCACCATGCTATCGGCGCCCTGATGCACGCGGTGTGTTGGACAAGT	1500
Dd	515	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal	534
OY	1501	ACGCGCATCATCCAGCGCATGTAGCGCCCGCGCTTCTGTACACACAGCCGAGCCGCGGAC	1560
Dd	535	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgSp	554
OY	1561	CTGGCGGACTACATCCGCATCCACGCTATCCCAAGCCCGCAAGCAGCAGCATGCTGGAG	1620
Dd	555	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuL	574
OY	1621	TACTTCAGGCGCACTGGGCGGTGAAACATGATGCATGCAGCACACCAGCACTGCTGAGAC	1680
Dd	575	TyrPheGlnAlaIleThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuIns	594

QY 1661 CTCCCTGACGAGCTGCGGCGGACATCGCATGCGACAGAGGCTGCTGACGCTG 1740  
 DB 595 LeuProAspGluLeuAlaAlaSerIleAlaMetHisLeuHisLysGluValLeuGlnLeu 614  
 QY 1741 CCACTGTTGAGGCGGCGGACGCGGCTGCTGCGGCGGACTGCTGCTGCGGCGG 1800  
 DB 615 ProLeuPheGluAlaAlaSerArgLysLeuAlaLeuSerLeuAlaLeuArgPro 634  
 QY 1801 GCCTTCTGACAGCGGCGGAGTACTCATCCACCAAGGCGATGCGCTGACGCTTAC 1860  
 DB 635 AlaPheCysTrpProGlyLysLeuLeuHisGlnGlyLysAlaLeuGlnAlaLeuTrp 654  
 QY 1861 TTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 DB 655 PheValCysSerGlySerMetGluValLeuLysGlyLysTrpValLeuAlaIleLeuGly 674  
 QY 1921 AAGGCGGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980  
 DB 675 LysGluLysPheLeuIleGlyCysGluLeuProArgGlyGluGlnValValAlaAla 694  
 QY 1981 GACGTGAGGCGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
 DB 695 AspValLysGlyLeuTrpTrpCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHis 714  
 QY 2041 AGCTTGGCGCTGACCCGAGCTTGGCCGCTTCACTGCTGCTGCTGCTGCTGCTG 2100  
 DB 715 SerLeuAlaLeuTrpProGlyPheAlaProArgPheSerArgLysLeuArgGlyLeu 734  
 QY 2101 AGCTACAACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 DB 735 SerTrpAsnLeuGlyAlaGlyGlyLysSerAlaGluValAspTrpSerLeuSerCyl 754  
 QY 2161 GACAAATACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220  
 DB 755 AspAsnTrpLeuMetSerTrpLeuGlnGlnLysGlyTrpAspGlyGlnGlnLysPro 774  
 QY 2221 GTCTCCCGACCCCGCTGATGAGCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCT 2280  
 DB 775 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysTrp 794  
 QY 2281 TCATCTCAGCTCCCAAGCTGCTATCCCACTGCAAGACAGCCCGCTGCTGCTAG 2340  
 DB 795 SerSerSerAlaAlaLysLeuLeuSerProArgPheTrpAlaProArgProArgLys 814  
 QY 2341 GGCAGAGGAGGCGGCGGCGGCGGCGGCTTGAAGGCTGAGGCTGCGCTGCTGCC 2400  
 DB 815 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAla 834  
 QY 2401 CCAAGGCGCTAGAGGCGCTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2460  
 DB 835 ProArgAlaLeuGlnGlyLeuAlaGlyLeuProMetProTrpAsnValProProAsp 854  
 QY 2461 AGCCCGAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 DB 855 SerProArgValValAspGlyIleGlyLysAspGlyCysGlySerAspGlnPolysPhe 874  
 QY 2521 TTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2580  
 DB 875 PheArgValAlaGlyLysSerGlyProGlyLysSerSerSerProSerProGlyPro 894  
 QY 2581 GGCCTGCTACAGCTTCCCATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2640  
 DB 895 GlyLeuLeuTrpValProHisGlyProSerGluAlaArgAsnTrpHisAspLys 914  
 QY 2641 CTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700  
 DB 915 LeuArgGlnAlaValTrpTrpLeuSerGlnGlnValLeuGlnMetArgGlnGlnLys 934  
 QY 2701 TCACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2760  
 DB 935 SerLeuArgGlnAlaValAlaGlnLeuValLeuAlaProHisArgGlnGlyProCysPro 954  
 QY 2761 GCATCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2820

DB 955 AlaSerGlyGlnGlyProCysProAlaSerTrpSerGlyLeuLeuGlnProLeuGlyVal 974  
 QY 2821 GACACTGGGGGATCCTCTCTACTGCTGCGAGCCCGGCGGCTGCTGCTGCTGCTG 2880  
 DB 975 AspTrpGlyAlaSerSerTrpCysLeuGlnProProAlaGlySerValLeuSerGly 994  
 QY 2881 TGGCCCGACCTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2940  
 DB 995 TrpProHisProArgProGlyProProProProLeuMetAlaProTrpProTrpLysPro 1014  
 QY 2941 GCGTCTCAGAGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3000  
 DB 1015 AlaSerGlnSerSerProTrpProArgAlaTrpAlaPheTrpTrpSerHisAsp 1034  
 QY 3001 GAGCCCGCTGCTCAGGAGACCTGCTGCTGAGCCGAGCCGCGGCGGCGGCGGCGG 3060  
 DB 1035 GluProProAlaSerGlyAspLeuGlySerGlnProSerTrpProAlaSerProPro 1054  
 QY 3061 TCTGAGGAAGGCGCTAGAGACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3120  
 DB 1055 SerGlnGlnGlyAlaArgTrpGlyProAlaGlnProValSerGlnAlaGlnAlaTrp 1074  
 QY 3121 ACTGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3180  
 DB 1075 ThrGlyGlnProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSer 1094  
 QY 3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240  
 DB 1095 GluMetValLeuIleGlyCysHisGlySerGlyTrpValGlnTrpTrpGlnGlnGly 1114  
 QY 3241 ACAGGCGTC 3249  
 DB 1115 ThrGlyVal 1117  
 RESULT 2  
 ID 089047 PRELIMINARY; PRT; 1087 AA.  
 AC 089047;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Euk channel 2 (Potassium channel).  
 GN Euk2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COX2;  
 RA Engeland B., Neu A., Ludwig J., Roeper J., Pongs O.;  
 RT "Identification of three rat potassium channel genes homologous to D.  
 RL melanogaster elk.";  
 RN Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 120-273 FROM N.A.  
 RX MEDLINE=98382545; PubMed=9714851;  
 RA Shi W., Wang H.S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,  
 RT Dixon J.E.;  
 RL "Cloning of a mammalian elk potassium channel gene and EAG mRNA  
 distribution in rat sympathetic ganglia.";  
 RN J. Physiol. (Lond) 511:675-682(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRN1;  
 RX MEDLINE=99386988; PubMed=10455180;  
 RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furutachi K.;  
 RT "New ether-a-go-go K+ channel family members localized in human  
 RL telencephalon.";  
 RN J. Biol. Chem. 274:25018-25025(1999).  
 DR EMBL; AF007627; CAA07586.1; -;  
 DR EMBL; AF073892; AAC61522.1; -;



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Db 581 LeuGlnLeuProLeuPheGlnAlaIleSerArgGlyCysLeuArgAlaLeuSerLeuAla 600
QY 1792 CTGGGGCCCCGCTTCTGACAGCGCGGAGTACCTCATCCACCAAGGCGATCCCTGCAG 1851
Db 601 LeuArgProAlaPheCysThrProGlyIuTyLeuIleHISGlnGlyAspAlaLeuGln 620
QY 1852 GCGCTCTACTTGTGCTGCTGGCTCCAGGAGGCTCTCAAGAGGTGGACCGCTGCTGCC 1911
Db 621 AlaLeuTyPheValCysSerGlySerMetGluValLeuGlyGlyThrValLeuAla 640
QY 1912 ATCTAGGAGGAGGCGACCTGATCGCTGTGAGTGGCCCGCGGAGGAGGAGGAGGAG 1971
Db 641 IleLeuGlyIysGlyAspLeuIleGlyGlyGluLeuProGlnArgGluGlnValIlys 660
QY 1972 GCCAATGCCAGCTGAGAGGGGCTGACTGCTGCTGAGTGTCTGAGCTGAGCTGGC 2031
Db 661 AlaAsnAlaAspValIysGlyLeuThrTyrcysValLeuGlnCysLeuGlnLeuAlaGly 680
QY 2032 CTGACAGCAGACCTTGGCTGTACCCGAGTTTGGCCCGCTTCAAGTGGCTGCCA 2091
Db 681 LeuHISGlnSerLeuAlaLeuTyPheGlnPheAlaProArgPheSerArgGlyLeuArg 700
QY 2092 GGGAGCTCAGCTCAACCTGGGTGCTGGGAGGCTGTGACAGAGGTGACACAGCTCC 2151
Db 701 GlyIuLeuSerTyPheAsnLeuGlyAlaGlyIysValSerAlaGlnValAspThrSerSer 720
QY 2152 CTGAGCGGCGACATATACCTTATGCTCCAGCTGGAGGAGGAGGAGGAGGAGGAG 2211
Db 721 LeuSerGlyAspAsnThrLeuMetSerThrLeuGlnGlyIysGlyIuThrAspGlyIuGln 740
QY 2212 GGGCCACAGCTCTCCAGCCGACCTGATGAGCCCTCCAGCCCTGCTGCTGCCCTGGC 2271
Db 741 GlyIuThrIleSerProAlaProAlaAspIuProSerSerProLeuLeuSerProGly 760
QY 2272 TGCACCTCTCATCTCTAGCTGCCAGCTGCTATCCCAAGCTGCAAGACACCCGGGCT 2331
Db 761 CysThrSerSerSerSerAlaAlaIysLeuLeuSerProArgGlyThrAlaProArgPro 780
QY 2332 CGCTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2391
Db 781 ArgLeuGlyIysArgGlyIysArgProSerArgGlyIysValLeuIysProGlnAlaGlyPro 800
QY 2392 TCTGCTCTCCCGGCTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2451
Db 801 SerAlaIleProArgGlnLeuAspGlyIysLeuIuLeuProMetProTPAsnValPro 820
QY 2452 CCAAGATCTGAGCCCGAGGAGTATGATGATGATGATGATGATGATGATGATGATG 2511
Db 821 ProAspLeuSerProArgValIysAlaGlyIleGlnAspGlyIysGlySerAspGlnHis 840
QY 2512 AATTTCTTTCCGCGTGGGCGAGCTGCGCCCGGAGATGATGATGATGATGATGATG 2571
Db 841 LysPheSerPheArgValIysGlnIserGlyProGlnCysSerSerSerProSerProGly 860
QY 2572 CCAGAGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2631
Db 861 ThrGlnSerIysLeuLeuThrValProLeuValProSerGlnAlaArgAsnThrAspThr 880
QY 2632 CTGACAGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2691
Db 881 LeuAspIysLeuArgGlnAlaValIleGlnLeuSerIuGlnValIleGlnMetArgGln 900
QY 2692 GGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2751
Db 901 GlyLeuGlnIserLeuArgGlnAlaValIleGlnLeuIleValProGlnIysGlnGlyGln 920
QY 2752 TGGCTTGGGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2811
Db 921 CysProArgValSerGlyIysGlyIysProCysProAlaThrAlaSerGlyLeuLeuGlnPro 940
QY 2812 CTGTGTGTGAGACATGGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2871
Db 941 LeuArgValAspThrGlyIysSerSerTyrcysLeuGlnProProAlaGlySerValIleu 960

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QY 2872 AGTGGACTTGGGCGCCACCTGCTCCGGG---CTCTCTCCCTCAAGGACCTGGCCC 2928
Db 961 SerGlyThrTriProIleHisProArgGlyIysProProProLeuMetAlaProTriPro 980
QY 2929 TGGGGTCCCGCAGCGCTCAGAGCTCCCGCTGGGCTCGAGCCACAGCTTCTGAGCTCC 2988
Db 981 TrpGlyProProAlaSerGlnIserSerProTriProArgAlaThrAlaLeuTriPheSer 1000
QY 2988 ACCTGAGTCAAGAGCCCGCTGCTCAGAGACCTTGTCTGAGCCAGACCCCTGCC 3048
Db 1001 ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020
QY 3049 TCCCGCTCCCTTCTGAGAGGAGGCTAGACTGGGCGCCGAGAGCTTGTGAGCCAGCT 3108
Db 1021 SerProProProProGlnIuGlyAlaArgThrGlyThrProAlaProValSerGlnAla 1040
QY 3109 GAGCTACAGCAGCTGAGAGGAGCCGACAGGAGTCAAGGAGGAGGAGGAGGAGGAGG 3168
Db 1041 GluAlaThrSerThrGlyIuProProProGlySerGlyArgAlaLeuProTriPasp 1060
QY 3169 CCCACAGCTGAGAGTGGCTTATGGCTGCTCCATGCTGCTGAGCAGACAGTCCAGTGG 3228
Db 1061 ProHISserLeuGlnMetValLeuIleGlyCysHISGlyProGlySerValGlnTriPhe 1080
QY 3229 CAGGAGAGGAGCAGAGGAGGCTC 3249
Db 1081 GlnGlnGlnGlnGlyThrGlyVal 1087

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RESULT 3

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ID Q9WVJ0 PRELIMINARY; PRT; 1087 AA.
AC Q9WVJ0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ethier-a-90-go-like potassium channel.
GN KCNH3 OR ELK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99208772; PubMed=10191308;
RA Titus S.A., Ganetzky B.S., Robertson G.A., Trudeau M.C.,
RA Branchaw J.L.;
RT "Functional analysis of a mouse brain Elk-type K+ channel.";
RL J. Neurosci. 19:2906-2918(1999).
DR EMBL; AF109143; AAD40578.1; -.
DR MGD; MGI:1341723; Kcnh3.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS.
DR InterPro; IPR000014; PAS-assoc_C.
DR Pfam; PF00027; CNMP_binding.
DR Pfam; PF00520; Ion_trans.1.
DR Pfam; PF00785; PAC.1.
DR SMART; SM00100; CNMP.1.
DR SMART; SM00086; PAC.1.
DR SMART; SM00091; PAS.1.
DR TIGRFAMs; TIGR00229; sensory_box.1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW Ionic channel.
SO SEQUENCE 1087 AA; 117537 MW; EBSDE6B7BA651F8 CRC64;

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Alignment Scores:

Pred. No.:	Length:	1087
Score:	5416.00	1087
Percent Similarity:	96.418	Matches: 11
Best Local Similarity:	95.408	Mismatches: 35

Query Match: 88.95% Indels: 4  
DB: 11 Gaps: 2  
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DB 1 MetProAlaMetProGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
OY 61 CGCTTCAGCGGACGACAGTAATCTGCTGCGGACAGCCCGAGGTGGCGGCTCTTC 120  
DB 21 ArgPheAspGlyThrHisSerAsnPheValIleuGlyAsnAlaGlnValAlaIleuPhe 40  
OY 121 CCCGTTGCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 180  
DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaVal 60  
OY 181 AMGCAGCGGGGCTGCGCTCTCTCTTATGGCGCAGACACGAGCTGAGCTGCGCC 240  
DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerIleuValArg 80  
OY 241 CAACAGATCCGACAGGCGCTGAGCAGCAGCAAGAGTTCAGAGCTGAGCTGATCTGTAC 300  
DB 81 GlnGlnIleArgIleValAlaLeuAspGlnHisLysGlnPheLysAlaGlnLeuIleuTyr 100  
OY 301 CGAAGAGCGGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 101 ArgLysSerGlyLeuProPheThrPcysLeuLeuAspValIleProIleLysAsnGlnLys 120  
OY 361 GGGAGAGTGGCT 420  
DB 121 GlyGlnValAlaLeuPheLeuValSerHisLysAspIleSerIleThrLysAsnArgGly 140  
OY 421 GGGCGCGACAGATGGAGAGAGACAGGTGGCGCGCGCGCGATATGGCGCGAGCATCC 480  
DB 141 GlyProAspAsnThrLysGlnArgGlyGlyGlyArgArgGlyTyrGlyArgAlaGlySer 160  
OY 481 AAAGGCTTAATGCCAAGCGCGCGCGCGCGCGCGCGCGCTGCTTACCACTGCTGCGGAC 540  
DB 161 LysGlyPheAsnHisAlaSerArgArgSerArgAlaValLeuTyrHisLysSerGlyHis 180  
OY 541 CTGCAGACAGCG 600  
DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValAlaPheGlyGlnLysPro 200  
OY 601 AACTGCTGAGTACAAAGTAGCCCGCATCCGGAAGTGGCGCTTCACTCTGCTGCACTGT 660  
DB 201 AsnLeuProGlnTyrLysValAlaAlaIleArgLysSerProPheIleLeuHisCys 220  
OY 661 GGGGCACTGAGACCGACCGCGGATGGCTTCATCTGCTGCGCACTCTATGCTGCTGCT 720  
DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
OY 721 ACTGTGCGCTACAGCGTGTGTGAGACAGCAGCAGGAGCGCGCGCGCGCGCGCGCGCG 780  
DB 241 ThrValProTyrSerValCysValSerThrAlaArgIleProSerAlaAlaArgGlyPro 260  
OY 781 CCCAGGCTGTGACCTGCG 840  
DB 261 ProSerAlaLysAspLeuAlaValGlnValLeuPheIleLeuAspIleValLeuAsnPhe 280  
OY 841 CGTACACCAATTCGTGTCAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900  
DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
OY 901 CACTAGCTCACACCTGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaIleLeuProPheAspLeu 320  
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DB 321 HisAlaPheLysValAsnValTyrValGlyAlaHisLysLeuLysThrValArgLeuLeu 340

OY 1021 CGCTTGTCCGCTCTGCTTCCGCGGCTGACCGCGTACTGCGCACTACAGCGCGCTGCTGCT 1080  
DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValLeu 360  
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DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValThrPheTyr 380  
OY 1141 ATTGGCAGCGGAGATGAGAGACAGCAGCAATCCGAGCTCTGAGTATGGCTGCTGCTGCT 1200  
DB 381 IleGlyGlnGlnIleIleGlnLysSerGlnSerGlnLeuProGlnIleGlyThrProLeuGln 400  
OY 1201 GAGCTGGCG 1260  
DB 401 GlnLeuAlaArgArgLeuLeuThrProTyrTyrLeuValSerArgSerProAspGlyGly 420  
OY 1261 AACAGCTCGCGCGCGAGTACAACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320  
DB 421 AsnSerSerGlyGlnSerGlnLysCysSerSerSerSerGlyGlyGlySerGlnAlaAsnGly 440  
OY 1312 ACGGGCTGAGCTGCTGCG 1371  
DB 441 ThrGlyLeuGlnLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460  
OY 1372 TTGCGACAGCAGCGCTGACAGCAGCGTGGCGTTCGCGCGCGCGCGCGCGCGCGCGCG 1431  
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DB 481 GlnLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPhe 500  
OY 1492 GGGAGCTGAGCGCGCATCATCAGCGCGAGTACCGCGCGCGCGCGCTTCTGTCACAGCGCG 1551  
DB 501 GlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArg 520  
OY 1552 ACCGCGGACCTGCG 1611  
DB 521 ThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArg 540  
OY 1612 ATGCTGAGTACTTCCAGCG 1671  
DB 541 MetLeuGlnTyrPheGlnAlaThrTrpAlaValAlaAsnAsnGlyIleAspThrThrGlnLeu 560  
OY 1672 CTGCAGAGCTCCCTGACGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1731  
DB 561 LeuGlnSerLeuProAspGlnLeuArgAlaAspIleAlaMetHisLysHisLysGlnVal 580  
OY 1732 CTGCAGCTGCCACTGTTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1791  
DB 581 LeuGlnLeuProLeuPheGlnAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAla 600  
OY 1792 CTGCGCGCGCGCTTCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1851  
DB 601 LeuArgProAlaPheCysThrProGlyGlnTyrLeuIleHisGlnGlyAspAlaLeuGln 620  
OY 1852 GCCCTTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1911  
DB 621 AlaLeuTyrPheValCysSerGlySerMetGlnValLeuLysGlyGlyThrValLeuAla 640  
OY 1912 ATCTAGGAGAGGCG 1971  
DB 641 IleLeuLysGlyGlyAspLeuIleGlyCysGlnLeuProGlnArgGlnGlnValValLys 660  
OY 1972 GCCAATGCCGAGTGAAGGGGCTGACGTACTGCTCTGCAAGTGTCTGCACTGGCTGGC 2031  
DB 661 AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly 680  
OY 2032 CTGCAGACAGCTTGGCGCTTACCCGAGATTTGCGCGCGCGCGCGCTCAAGTGGCGCTCG 2091  
DB 681 LeuHisGlnSerLeuAlaLeuTyrProGlnPheAlaProArgPheSerArgGlyLeuArg 700  
OY 2092 GGGAGGCTCAGCTCAACCTGGGTGCTGCGGGAGGCTCTGCAAGAGTGGACACAGCTCC 2151

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QY 2212 GGGCCAGCGGCTCCCGACGCGCTGATGAGCCCTCCAGCCCTGCTGCTCCCTGGC 2271
Db 741 GlyHisThrLeuSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGly 760
QY 2272 TGCACCTCTCATACCTCAGCTGACAGCTGCTATCCCGACGTGACAGACACCCGGCCT 2331
Db 761 CysThrSerSerSerSerAlaAlaLysLeuLeuSerProAlaGlyThrAlaProAlaPro 780
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QY 2392 TCTGCTCCCCAGGCGCTAGAGGGGCTACGAGGCTCCCGCCATGCTAGATGAGCC 2451
Db 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProMetProThrAsnValPro 820
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Db 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly 860
QY 2572 CCAGAGCGGCGCTCTCACTGCTCCCATGGGCGGCGGAGGAGGAGGAGGAGGAGGAG 2631
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Db 1041 GluAlaThrSerThrGlyGluProProProGlySerGlyGlyArgAlaLeuProThrPasp 1060
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QY 3229 CAGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3249
Db 1081 GlnGluGlnGlyThrGlyVal 1087

RESULT 4
ID 096L42 PRELIMINARY; PRT; 1107 AA.
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DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Echer-a-90-90-like potassium channel 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmquist M.H.,
RT "A novel membrane potential-sensitive fluorescent dye improves cell-
RT based assays for ion channels."
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY053503; ARL15429.1; -
DR InterPro: IPR000595; cAMP_binding.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-associ_C.
DR InterPro: IPR000014; PAS_domain.
DR Pfam: PF00027; cAMP_binding; 1.
DR Pfam: PF00520; ion_trans; 1.
DR SMART: PF00785; PAC; 1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 1.
DR TIGRfams: TIGR00229; sensory_box; 1.
DR PROSITE: PS00042; cAMP_BINDING_3; 1.
DR Ionic channel.
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Score: 2529.50 Matches: 559
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Query Match: 41.54% Indels: 201
Gaps: 27

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QY 61 CGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 120
Db 21 ArgPheAspGlyThrHisSerAspPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
QY 121 CCGGTGCTACTGCTGATGAGGCTTGTGACCTCACGGGCTTCCCGGCTGAGGCTC 180
Db 41 ProIleValIlyCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60
QY 181 ATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
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QY 241 CAACAGATCCGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 81 LeuGlnIleGluLysSerLeuGlnGluGluThrGluPheLysGlyGluIleMetPheYr 100

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Db Glnasparalvalineleucylalaserphenylseryllethrinaspthrlyvalylle 140  
421 GGCCCGCAGAGTGAAGAGAGAGAGTGGTGGCGCGCGCATATGGCCGGGACAGATCC 480  
Db Thrprolineasparaglylasp-----lysvalylsargylserargala 156  
481 ---AAGGCTCAATGCCAACCGCGCGGAGCGCGCGCGCTCTACACCTGGCGG 537  
Qy Glnthrinleuaspseralalargylserargalaalvalleuthrhisileserly 176  
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538 CACCTGCAGAGAGAGCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597  
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658 TGTGGGCACTGAG 717  
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237 Valthrvalprotyrvalasparalysylpheleuaspasparleuaspaspar 256  
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257 ---Thrvalseraspasparalvalalvalleuaspasparleuaspasparleuaspas 275  
838 TTCGACACATGCTGCTTCAAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897  
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276 Phelethrleuaspasparaglylserleuaspasparaglylserleuaspaspar 295  
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1318 CTGAGAGTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377  
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Qy Valthrvalprotyrvalasparalysylpheleuaspasparleuaspasparleuaspaspar 1977  
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OY 2488 GACGGCTGTGGCTCGAGCAGCCAG-----TTCTCTTTCGGCTGGCGCAGTGTGGCCG 2544
Db 819 AspGlyAsnSerSerGlnLysSerGlnThrPheAspPheLysSerGlnArgIleArgSer 838
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OY 2965 CGAGCCACAGCTTCTGACCTCCACCTCAGACTCAGAGCCCTGCTCAGAGACTC 3024
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OY 3025 TGCCTACAGCCCAAGCCCTGCTCCCT----- 3054
Db 986 TyrHisSerProSerIleAsnArgLysThrProSerHisThrGlnValGlnGlnGlyHis 1005
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Db 1045 ValLeuPro-----SerArgSerGlnGlu-----GlySerPheSerGlnGly 1058
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Db 1059 ThrValSerSerPheSerLeuGlnAsnLeuProGlySerThrAsnGlnGlu 1075

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AC 088877;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Potassium channel.
GN ELKT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98382545; PubMed=9714851;
RA Shi W., Wang H.S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,
RA Dixon J.E.,
RT Cloning of a mammalian elk potassium channel gene and EAG mRNA
RT distribution in rat sympathetic ganglia.
RL J. Physiol. (Lond) 511:675-682(1998).
DR EMBL: AF061957; AAC61520.1;
DR InterPro: IPR000595; cNMP_binding.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR00700; PAS-assoC.C.
DR InterPro: IPR000014; PAS_domain.
DR Pfam: PF00027; cNMP_binding.1.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF00785; PAC.1.
DR SMART: SM00100; cNMP.1.
DR SMART: SM00086; PAC.1.
DR TIGRfams: TIGR00229; sensory_box.1.
DR PROSITE: PS50042; cNMP_BINDING_3; 1.
KW Ionic channel.
SQ SEQUENCE 1102 AA; 123230 MW; A135CC36E2E7F1A3 CRC64;

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Query Match: 41.30% Indels: 134
DB: 11 Gaps: 24

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Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
OY 61 CGCTTCAGCGGAGCAGCAAGTAACCTTGTGCGGCAACGCCAGAGTGCGGGCTTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
OY 121 CCGGTGTCTACTGCTGATGGCTTGTGTGACCTCAGAGGGCTTCCCGGGCTGAGTTC 180
Db 41 ProIleValIleTyrCysSerAspPheLysCysGlnLeuAlaGlyPheAlaArgThrGlnVal 60
OY 181 ATGCAGCGGGCTGTGCTGCTCTTCTTATGAGCCAGACACAGTCACTGCTGCC 240
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGlnThrAsnGlnLeuMet 80
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Db 81 LeuGlnIleGlnLysSerLeuGlnGlnIleValGlnPheLysGlyLileMerPheThr 100
OY 301 CGAAGAGCGGGCTCCGCTGTGCTGTCTGCTGATGTGATACCATTAAGATGAGAAA 360
Db 101 LysLysAsnGlyAlaProPheTyrCysLeuLeuAspIleValProIleLysAsnGlnLys 120
OY 361 GGGAGGTGCTCTCTCTCAGTCTTCACAGAGACATCAGCGAAGCAAGCAAGCAAGCA 417
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140

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Rt	J. Biol. Chem.	274	:25018-25025(1999).
DR	EMBL	AB022698	:BAA83592..1:-
DR	InterPro	IPR000595;	CNMP_binding.
DR	InterPro	IPR001622;	K+channel_pore.
DR	InterPro	IPR000636;	M+channel_1lg.
DR	InterPro	IPR001610;	PAC.
DR	InterPro	IPR000700;	PAS-asoc-C.
DR	InterPro	IPR000014;	PAS_domain.
DR	Pfam	PF00027;	CNMP_binding; 1.
DR	Pfam	PF00520;	ion_trans; 1.
DR	SMART	SM00100;	CNMP; 1.
DR	SMART	SM00086;	PAC; 1.
DR	SMART	SM00091;	PAS; 1.
DR	TIGRFAMs	TIGR00229;	sensory_box; 1.
DR	PROSITE	PS0042;	CNMP_BINDING_3; 1.
SO	SEQUENCE	1017 AA;	11693 MW; 4B480DFC75816A38 CRC64;
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Pred. No.:	7,71e-129	Length:	1017
Score:	2461.50	Matches:	538
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Query Match:	40.43%	Indels:	208
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OY	61 CGCTTCGACGGCACGCACAGTAATCTGCTGTGGCAAGCGCCAGGTGGCGGGCTCTC	120	
Dd	21 ArgPheAspArgLysThrHisSerAsnPhenLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe	40	
OY	121 CCCCGGCTCATCTGCTGTGATGGCTCTGTGTACCTACAGGCTTCTCCCGGGTAGGCTC	180	
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OY	181 ATGCAGCGGGGCTGCGCTGCTGCTCTTTATGGGGCCAGACACCAAGTGAAGTACCTGCTCCG	240	
Dd	61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGlnThrSerGluProAlaLeu	80	
OY	241 CAACAGATCCGCAAGGCCCTTGAGAGACACAAGAGTTCAGGCTGAGCTGATCTGTAC	300	
Dd	81 GlnArgLeuHisLysAlaLeuGlnGlyHisGlnGlnHisArgAlaGluIleCysPheTyr	100	
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Dd	101 ArgLysAspArgLysSerAlaPheThrProCysLeuLeuAspMetProIleLysAsnGluMet	120	
OY	361 GGGAAGTGGCTCTCTTCTTCAAGTCTCTCACAAAGACATCAACGGAACCAAGAACGAGG	420	
Dd	121 GlyGluValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly	140	
OY	421 ---GGCCCCGACAAATGGAAGGAACAAGTGGTGGCGCGCCGATATGGCCGGGACAGA	477	
Dd	141 LeuGlyProGln-----GlyLysArgGlyAspSerAsnHisGluAsn	154	
OY	478 TCCAAAAGCC-----TTCAATGCCAACCGGGCGGGCGAGCCGGGCC	516	
Dd	155 SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgArgSerArgThr	174	
OY	517 GTGCTTACACACTGTCCGGGACCTCGACAGAAGGACGCCCAAGGCAAGCAAGCTCAAT	576	
Dd	175 ValLeuHisAspGluThrGlyHisPheGlyArgArgGlyGlnGlyMetLysAlaAsn	194	
OY	577 AAGGGGTTGTTGGGGGAACAAACCACTGTGATGATGATCAAAAGTAGCCGCGACCGGAAG	636	
Dd	195 AsnAsnValPheGluProLysProSerValProIleTyrLysValAlaSerValGlyGly	214	
OY	637 TCGCCCTTCACTCTGTGGCACTGTGGGGCACTGAGACCACTGGGATGGCTTCAATCTG	696	

Db	215	SerArgCysLeuLeuLeuHisIstYserValSerIysAlaIleThrAspIleLeu	234
QY	697	CTCGGCACACTCTATGTGGCTGCTGCACCTGTGCCCTACAGCGGTGTGTGAGCACAGCACGG	756
Db	235	LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerGlyAspAsp	254
QY	757	GAGCCCACTGCCCGCGCGCGCGCCGCCACGCTGTGTGACCTGGCCGTGGAGTCTCTTC	816
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QY	817	ATCCTTGACATTGTGCTGAATTTCCGTACCAATTCGTGTCCAAAGCGGGCCAGCGTGGG	876
Db	275	IleLeuAspIleIleLeuAsnPheArgThrTyrValSerGlnSerGlyGlnValIle	294
QY	877	TTTGGCCCCAAATTCATTTGGCTCCACCTGCACGTGCACACCACTGGTGTCTCGCTGATGCATC	936
Db	295	SerAlaProArgSerIleGlyLeuHisIstIyrLeuAlaThrThrPhePheIleAspLeuIle	314
QY	937	GCAGCGCTCCCTTTGACCTGTGTACATGCTTCGAAGTCAAGCTGACTACTTCGGGGCCAT	996
Db	315	AlaAlaIleuProPheAspLeuLeuTyrIlePheAsnIleThrValIhrSerLeuValHis	334
QY	997	CTGTGAAAGACGGGTGGCCTGTGTGCGCTGCCTGCTGCGGCTGTTCCGCGCTGACCGGTAC	1056
Db	335	LeuLeuLysThrValArgLeuLeuArgLeuLeuArgLeuLeuGlnIstLeuGlnArgTyr	354
QY	1057	TGCGAGTACAGCGCGCTGTGTGTGTGACACTGTCTATGTCGCGGTTCGCGCTCGCGCAC	1116
Db	355	SerGlnCysSerAlaValIleuThrIleuMetSerValPheAlaLeuLeuAlaHis	374
QY	1117	TGGGTCGCTGGCTGTGGTTTACATTTGGCCACGGGGAGATGAGAGCGCAATCGAG	1176
Db	375	TrpMetAlaCysIleThrTyrValIleGlyArgGlnMetIleuAlaAsnAspProLeu	394
QY	1177	CTGCGTAGATTGGCGGTGGCTGCGAGGATGGCCCGGACGTGAGACTCCCTACTACCTG	1236
Db	395	LeuThrAspIleGlyThrPheuHisGlnIleGlyLysArgLeuIleValProTyr	412
QY	1237	GTTGGCGCGAGCGCACCTGGAGGAACAGCTCCGGCCAGAGTACAACCTGCACAGCAGC	1296
Db	412	-----	412
QY	1297	AGCGAGGCCACGGGAGCGGGGGCTGAGCTGTGGGGCGGCCGTGCGCAGCGCCTAC	1356
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QY	1357	ATTCACCTCCCTTACTTTCGCACCTCAGCAGCCTTCACACAGCGTGGGCTTCGGCAACGTTC	1416
Db	427	IleAlaAlaLeuTyrPheThrIleuSerSerLeuThrSerValGlyPheGlyAsnValCys	446
QY	1417	GCCAAACGGCACCCGAAAGATCTTCATCTGCACCACTGTCACATGGTCATGGCGGCCATG	1476
Db	447	AlaAsnThrAspAlaGlnLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet	466
QY	1477	CACGGCGTGGTGTGGGAACGTGAGCGGCATATCAGCGGCATGATCCGCGCGCGCTTT	1536
Db	467	HisAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer	486
QY	1537	CTGTACACACAGCGCAGCGCGACCTGCGGACGTACATCCGATCCACAGCTATCCCAAG	1596
Db	487	LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg	506
QY	1597	CCCGTCAAGCGAGCGATGCTGAGTACTTTCACAGGCCACCTGGGCGGTGAACATGGCATC	1656
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Db	21	ArgPheAspGlyThrHisSerAsnPheLeuAlaAsnAlaGlnGlyProValGlyPhe	40
QY	121	CCCGAGCTACTGCGTCGATAGGCTTCGTGTACCTCAGCGGCTTCTCCCGGCTGAGTCC	180
Db	41	ProIleValIleTyrSerSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal	60
QY	181	ATGCAAGCGGGGTGAGCGCTGCTCTCTTATATGGCCAGCAACCAAGTACGACTGTCGCC	240
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QY	700	GCCACACTATGTGGCTGTACTGTGCTCCCTTACAGCGCTGTGTGTAGCACAGCACGGAG	759
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Db	257	ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGlnMetLeuPheIle	276
QY	820	CTTGACATTTGGTGAATTTCCGACACATCTGTGTCGCAAGTCGGGCGGACAGTGGTTT	879
Db	277	LeuAspIleIleLeuAsnPheArgThrThrTyrValSerIleSerIleGlyAlaValSer	296
QY	880	GGCCCAAGATCCATTTGCTCCATACAGTACACCACTGGTCTGTGTGATGATGATCGGA	939
Db	297	AlaProIleSerGlnIleGlyLeuHisTyrIleAlaIleThrIlePhePheValAspLeuIleAla	316
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Db 569 LeuSerLeuHisIleLysThrSerPheCysAlaProGlyGlnLeuLeuArgArgGly 588
QY 1840 GATCCCTGCGAGCGCTTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1899
Db 589 AspAlaLeuGlnAlaIleLysTyrValCysSerGlySerLeuGlnValLeuArgAspAsn 608
QY 1900 ACCGTGCGCGCATCTGAGAGGAGCGGAGCGGAGTGCCTGAGCTGAGCTGCGCGCGGAG 1959
Db 609 ThrValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGlnLeuGly 628
QY 1960 CAG-----GTGTAAGGCCAAATGCCGAGCTGAAGGGGCTG 1995
Db 629 GlnGlnProGlyAlaGlyAlaGlyCysValLeuLysThrSerAlaAspValLysAlaLeu 648
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QY 2056 CCCGAGTTGGCCCGCGCTTACGTGCGCTCCGAGGGGAGCGGAGCTACAACTGGGT 2115
Db 669 ProGlnTyrValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPheAsnLeuArg 688
QY 2116 GCTGGGGA----- 688
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QY 2134 GAGGTGACACCACTCCCTGACGCGCGCGAGCAATACCTTATGTCACAGCTGAGAGAGAG 2193
Db 709 ArgSerAspThrLeuGlnLysSerSerAspLysThrLeuProSerIle-----Thr 725
QY 2194 GAGACAGATGGGAGAGAGCGCGCCAGCGTCTCCAGCGCCAGCTGATGAGCCCTCAGC 2253
Db 726 GlnThrGlnIle-----GlyMetGlnProGlyAlaGlySerLysProArgArg 741
QY 2254 CCCCTGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2301
Db 742 ProLeuLeuProAsnLeuSerProAlaArgProArgLysLeuValSerLeuLeu 761
QY 2302 -----CTATCCCACTGCA 2316
Db 762 GlyGlnGlnLeuProProPheSerAlaLeuValSerSerProSerLeuSerPro----- 779
QY 2317 ACAGCACCCCGCGCTGTAGTGGCAGAGGAGCGGAGCGGAGCGGCTTGAAG 2376
Db 780 ---ThrProSerProAlaLeuAlaGlyArgGly----- 789
QY 2377 GCTGAGGCTGCCCTCT-----GTCGCCCAACGGCGCTAGAGGG 2418
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QY 2419 ---CTACGGCTGCGCGCCCATGCAATGTCGCGCCCATGTCAGCCCGAGGTAGTA 2475
Db 808 GlnLeuLeuThrProProLeuGlnGlyThrPheGlyProProAspLeuSerProArgIleVal 827
QY 2476 GATGGCATTGAAAGCGGCTGTGGC---TCGAGACCAACCAATCTTCTTCCGCGTGGC 2532
Db 828 AspGlyIleGlnLysAspSerSerAsnThrAlaGlnAlaProThrPheArgPhe----- 844
QY 2533 CAGTCTGCGCGGAAATGACAGCAGCGCCCTCCCTGACACAGAGCGGCTGCTGACT 2592
Db 845 SerLysArgProGlnProThrArgThrArgSerGlnAlaProLeuSer----- 860
QY 2593 GTTCCCATGGGCGCGAGGAGGCAAGAAC-----ACAGACACTGACACACTTCGG 2646
Db 861 -----GlyProArgLeuSerArgGlnLeuAlaThrGlnAlaAlaGlnGlnValLys 877
QY 2647 CAGCGGTGACAGAGCTGTGACAGAGTGTGACAGATGCGGAGAGGAGTCACTACT 2706
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Db 898 SerArgGlnLeuArgGlnValMet----- 905
QY 2767 GGAAGAGGCGCGTGGCCAGCAGCACTCCGCGCTTGTGACAGCTTGTGTGAGACT 2826
Db 906 -----GlyLeuLeuGlnAlaArg----- 911
QY 2827 GGGGATCTCTCTACTGCTGCTGACGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2886
Db 912 -----LeuGlyProProSer----- 916
QY 2887 CACCTGCTCGGGGCGCTCTCCCTCATGAGACCTGCGCTGCGCGCGCGCGCGCGCTCT 2946
Db 917 HisPro-----ProAsp-SerThrThrProAspLeuProCysProHis----- 931
QY 2947 CAGAGCTCCCGCTGCGAGCCAGACCTTGTGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAG 3004
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QY 3004 ----- 3004  
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 AC 089048;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Elk channel 1.  
 GN ELK1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cortex;  
 RA Engeland B., Neu A., Ludwig J., Roeper J., Pongs O.;  
 RT "Identification of three rat potassium channel genes homologous to D.  
 RT melanogaster elk.";  
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ007628; CAA07587.1; -  
 DR InterPro: IPR000595; cNMP\_binding.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR000700; PAS\_assoc.C.  
 DR InterPro: IPR000014; PAS\_domain.  
 DR Pfam: PF000027; cNMP\_binding; 1.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR Pfam: PF00785; PAC; 1.  
 DR SMART: SM00100; cNMP; 1.  
 DR SMART: SM00086; PAC; 1.  
 DR SMART: SM00091; PAS; 1.  
 DR TIGRFAMs: TIGR00229; sensory\_box; 1.  
 DR PROSITE: PS50042; cNMP\_BINDING\_3; 1.  
 SQ SEQUENCE 1017 AA; 111433 MW; FDFD7C3E67650C98 CRC64;  
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 Percent Similarity: 60.00% Conservative: 131  
 Best Local Similarity: 48.14% Mismatches: 244  
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 QY 61 CGCTTCAGCGGACGACAGTACTGCTGGGCAAGCCCGGCGGGGCTCTTC 120  
 Db 21 ArgPheAspGlyThrHisSerAsnPheLeuAlaAsnAlaGlnGlyProArgGlyPhe 40  
 QY 121 CCGGTGGTACTAGCTCTGATGCTTGTGACCTCAGCGGCTTCCCGGGCTGAGGTC 180  
 Db 41 ProIleValIleTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyAlaThrGluVal 60  
 QY 181 ATGACGGGGGCTGCTGCTCTTCCTTATGGGCGACAGACACAGTGAAGCTGCTGGC 240

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 QY 361 GGGAGAGTGGCTCTTCTTACTGCTCTACAGAGACATCAGCAAAACCAAGAACCGAGG 420  
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 QY 421 -----GGCCCGACAGATGAGAGAGACAGGTGTGGCGCGCGC 459  
 Db 141 LeuGlySerProGlyIleHisGlyAspAsnAsnHisGlnLysAsnSerLeuGlyArg--- 159  
 QY 460 CGATATGGCCGCGACAGATCCAAAGGCTTCAATGCCAACCGGGCGGCGCGCGCGCTG 519  
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 QY 520 CTCTACACCTGTCCGCGGACCTGACAGAGACCCCAAGGAGGACAGACAGCTCAATTAAG 579  
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 QY 1240 GGCAGGAGGCGAGCTGAGGAGAACAGCTCGGCGCAGAGTGAACATGACAGACAGCAGC 1299  
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QY 1300 GAGGCCAGCGGAGGCGGCTGAGCTGCGGGGCGCCGCTGCGGAGCGGCTGACATC 1359  
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 QY 1960 CAG-----GTGGTAAAGGCCAATGCCAGCTGAGAGGCGCTG 1995  
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 DB 912 -----LeuGlyProProSer----- 916  
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 ID Q23974 PRELIMINARY; PRT: 1284 AA.  
 AC Q23974;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative potassium channel subunit (PAG-like K<sup>+</sup>) channel protein).  
 GN ELK OR CG5076.

Db	21	ArgPheAsnArgLysThrHisSerAsnIleuValLeuValAsnIleValAsnGly----	Asn	39
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Db	40	ProIleValTyrCysSerAspGlyIleValAsnIleuThrGlyTyrSerAlaIleGlnIle		59
OY	181	ATGACAGCGGGGCTGGCTGCTGCTTCTGCTTATGAGGCGACAGCAAGCTAGAGCTGCTGAC		240
Db	60	MetGlnLysGlyCysSerCysHisPheIleuTyrGlyProAspThrLysGlnGlnHisLys		79
OY	241	CAACAGATCCGACAGGCGCTGGACAGACAGCAAGAGTTCAAGGCTGAGCTGATCTGTAC		300
Db	80	GlnGlnIleGlyLysSerLeuSerAsnLysMetIleuLysLeuGlnIleValIlePheTyr		99
OY	301	CGGAAGAGCGGGCTCCGCTTGTGCTGCTGCTGCTGATGATGATACCCATAAAGATAGACAA		360
Db	100	LysLysGlnGlyAlaIleProIleThrPcysLeuIleuPheAspIleValIleProIleLysAsnGlnLys		119
OY	361	GGGAGAGTGAGCTCTCTCTCTATGCTCTGACAAAGACATCAGCGAAACAG-----		411
Db	120	ArgAspValIleuPheIleuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu		139
OY	411	-----		411
Db	140	MetAsnValAsnGlnGlyLysAspSerValPheAlaIleuThrAlaIleuGlyAla		159
OY	412	-----AACCGAGG		420
Db	160	ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLysLeuProGlyLeuGly		179
OY	421	GGCCCC-----GACAGATGGAAGAGACAGACGTGTGTGGCGGCGCGATGTGGCCGG		471
Db	180	GlyProIleAlaSerAspGlyLysThrGlnIleAlaGlyLysLysAsnIleuAspValPro		199
OY	472	GCAAGATCCAAAGGCTTCAATGSCAAACGGCGGCGAGCCCGGCTGCTTACACATG		531
Db	200	Ala-----GlyCysAsnMetGlyArgGArgSerArgAlaIleuLysGlnIleu		216
OY	532	TCCGGGACCTGGAGAAAGCAGCCCAAGGC--AACACAAAGCTCAATAGGGG-----		582
Db	217	SerGlnHisTyrLysProGlnLysGlyGlyValLysThrLysLeuLysGlnLysAsn		236
OY	583	---GTGTTTGGGAGAAACCAAACTTGCGAGTACAAAGTAGCCGCCATCCGGAAGTGC		639
Db	237	PheMetHisSerThrGlyAlaIleProIleProGlyTyrLysThrGlnSerLeuLysSer		256
OY	640	CCCTTCATCTGTGTGCACGTGGGCGACAGACAGCCACACCTGGAGAGCTTCAATCCGTC		699
Db	257	ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleThrAspTrpValIleuVal		276
OY	700	GCCACACTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGACACAGCAGCGGAG		759
Db	277	AlaThrPheTyrValAlaIleuMetValProTyrAsnAlaIlePheAlaLysAlaAspArg		296
OY	760	CCCAAGCGCGCGCGCGCGCCAGCGCTGTGACACTGCGCGTGGAGAGCTCTTTCATC		819
Db	297	GlnThr-----LysValSerAspValIleValGlnAlaIleuPheIle		310
OY	820	CTTGACATGTGTGAATTTCCGTACACAACTCGTGCCAAATCGGCGGCAAGTGAGTTT		879
Db	311	ValAspIleIleLeuAsnIlePheArgThrThrPheValSerArgLysGlyIleValValSer		330
OY	880	GCCCAAAAGTCCATTTGGCTGCACATAGCTACACACCTGGTCCCTGAGATGATCGCA		939
Db	331	AsnSerLysGlnIleAlaIleAspTyrIleuArgGlyTyrPheAlaIleuAspIleuAla		350

OY 1048 GACGGTACTGCGAGTACAGCCCGTGGTGTGACACTGTCATGGCCCTGTTCGCCG 1107  
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DB 409 AlaAlaHisThrLeuAlaCysIleThrValIleAlaValIleGluIleu----- 426  
OY 1168 GAATCGAGCTGGCTGAG-----ATTGGCTGGCTGACAGAGCTGGCGCCGACTGGAG 1221  
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DB 427-----TrpPheProGlnSerAsnIleGlyTrpLeuGlnLeuMetAlaGluArg----- 442  
OY 1222 ACTCCCTACTACTGTGGTGGCCGAGCCAGCTGAGGAGAACATCCGGCCAGACTGAC 1281  
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DB 442----- 442  
OY 1282 AACTGAGAGCAGCAGCAGCCAGCCAGGAGCGGCTGAGACTGCTGGCGGCCGCTGC 1341  
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DB 443-----LysAsnAlaSerValAlaIleLeuThrAlaGlu----- 454  
OY 1342 CTCGGCAGCGCCCTACATCACTCCCTCTACTGCACTGCACTGCACTGCACTGCGG 1401  
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DB 455-----ThrySerThrAlaLeuThrPheThrPheThrSerLeuThrSerValGly 471  
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OY 1462 ATCGCGCCCTGATGACAGCGGTGTGTGGAACTGACGGCCATCATCAGCGCATG 1521  
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DB 492 IleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIleIleGlnArgMet 511  
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OY 1642 GTGACACATGGCATCGACACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1701  
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DB 552 LeuSerHisGlyIleAspIleThrGlnThrLeuArgGlnPheProGlnGlnLeuArgGly 571  
OY 1702 GACATGCCATGACACTGACACAGAGAGTCTGCACTGCACTGTTGAGCGGCCAGC 1761  
|||||  
DB 572 AspValSerMetHisLeuHisArgGlnIleLeuGlnLeuProIlePheGlnAlaSer 591  
OY 1762 CGCGGCTGCGTGGGAGACTGTCTGGCCCTGGCGCCGCTGTGACCGCGGCGAG 1821  
|||||  
DB 592 GlnGlySerLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu 611  
OY 1822 TACCTCATCCACCAAGCGATGCTGCAAGCCCTCTACTTTGTCTGTCTGGCTGCTG 1881  
|||||  
DB 612 TyLeuIleHisLysGlyAspAlaLeuAsnThrIleThrLysCysAsnGlySerMet 631  
OY 1882 GAGGTGCTCAAGGAGGAGCAGCTGCTGCACTGCTGAGGAGGAGGAGGAGGAGGAGT 1941  
|||||  
DB 632 GluValIleLysAspAspMetValAlaIleLeuGlnLysGlyAspLeuValGlySer 651  
OY 1942 GAGCTG----- 1947  
DB 652 AspIleAsnValHisLeuValAlaThrSerAsnGlyMetThrAlaThrThrAsnSer 671  
OY 1948 CCGCGCGGAGCAGAGTGTAAAGCCCAATGCCAGCTGAAAGGCTGACGTACTGCTC 2007  
|||||  
DB 672 AlaGlyGlnAspValValValArgSerSerSerAspIleLysAlaLeuThrThrLysAsp 691  
OY 2008 CTCGAGTCTGCGAGCTGAGCTGCGCTGCAACAGCAGCTGGGCTTACCCGAGTTGCC 2067  
|||||  
DB 692 LeuLysCysIleHisMetGlyGlyLeuValGluValLeuArgLeuArgProGlnIleu 711

OY 2068 CCGCGCTTACGTGCGCTCCGAGGAGCTCAGTACACTGCTGGGAGGAGC 2127  
|||||  
DB 712 GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGlnIleu 731  
OY 2128 TCTGACAGCTGACACACAGC-----TCCCTAGCGCGGCGACATACC 2169  
|||||  
DB 732 AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGlnAspArgGlu 751  
OY 2170 CTATTGTCACAGCTGAG-----GAGAGGAGACAGATGGGAGGAGGAGC 2214  
|||||  
DB 752 AsnArgGlnGlnAlaGlnGlnGlyGlyLysGlyGlnLysGlnAsnGly-----Gly 769  
OY 2215 CCC-----ACGCTCTCCCAAGCCCGCCAGCTGATGAGCCCTCC 2250  
|||||  
DB 770 ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 789  
OY 2251 AGCCCGCTGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2310  
|||||  
DB 790 SerProLeuLeuGlyMetGly-----SerPro 798  
OY 2311 CGTGAACAGCAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2370  
|||||  
DB 799 Arg-----AsnGlnArgLeuHisGlnArgGly----- 807  
OY 2371 TTGAAGCTAGGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2430  
|||||  
DB 808-----ArgSerLeuIleThrLeuArg----- 814  
OY 2431 CCATGCTGATGATGTGCCCCAGATCTGAGCCCGAGGCTAGATGATGATGATGATGATG 2490  
|||||  
DB 815-----GlnThrAsnLysArgHisArgHisArgHisArgHisArgHisArgHis 825  
OY 2491 GCGTGTGCTCGACACAGCCCAAGTCTCTTCCGCTGGGCGCAGTGTGGCCGGAATGT 2550  
|||||  
DB 826 AlaCysSerLeuAspArgGlySerPhe----- 834  
OY 2551 AGCAGCAGCCCTCCCTGACACAGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2610  
|||||  
DB 835-----GlnGlnProGlnProLeuGlnGlnIleu-----GlnSer 845  
OY 2611 GAGCGAAGAAACACAGACACTGACAGAGTGGGAGGCGGTCAGACAGCTGTGACAG 2670  
|||||  
DB 846 SerGlyGlyLysArgProSerLeuGlnArgLeuAspSerGlnValSerThrLeuHisGln 865  
OY 2671 CAGGTGCTGACAGCGGAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2730  
|||||  
DB 866 AspValAlaGlnLeuSerAlaGlnValArgAsnAlaIleSerAlaLeuGlnGlnMet 884  
OY 2731 GCGCCCCACAGGAGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2790  
|||||  
DB 885-----ThrPhe 886  
OY 2791 ACCTCGGCTTGTGACAGCTGTGTGTGTGACACTGCGGCACTCCTTACTGCTGAG 2850  
|||||  
DB 887 ThrSerAsnAlaMet-----ThrSerHisSerSerLeuLysPhe--- 899  
OY 2851 CCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2904  
|||||  
DB 900 ProProAlaArgSerIleProAsnIleSerGly--ValAlaLeuThrArgSerGlyVal 919  
OY 2905 CCGTCCCTCAGGAGCAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2964  
|||||  
DB 919 AlaValGlnHisGlyLeuMetGly--GlyValLeuAlaAlaLeuLeu--AlaAlaLeu 937  
OY 2965 CGAGCCACAGCTTGTGACAGCTGACACT-----CAGACTCAGAGCCCGCTGCG 3012  
|||||  
DB 937 GlnArgSerSerSerHisProProGlnValThrGlyArgAspValGlnLeuProThrSe 957  
OY 3013 TCAGAGACCTGCTGCTGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3052  
|||||  
DB 957 rAsnThrAlaSerSerLysAlaProSerProValGlnPro 970

RESULT 10

09V899	PRELIMINARY;	PRT;	1311 AA.
ID	09V899		
AC	09V899;		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)		
DE	ELK protein.		
GN	ELK OR CG5076.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
OX	NCBI_taxid=7227;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN-BERKELEY;		
RC	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,		
RA	Abrita J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Bernou B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck Y., Brokstein P., Brotlier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Centler A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K.C., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,		
RA	Glaser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Gooden A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,		
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,		
RA	Jaitani M., Kailush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacielb J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spieler E., Spradling A.C., Steplaton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zhang X.H., Zhong F., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RT	"The genome sequence of Drosophila melanogaster."		
RL	Science 287:2185-2195(2000).		
DR	EMBL; AE003801; AAF57772.1; -		
DR	EMBL; FBgn0011589; elk.		
DR	InterPro: IPR0000595; CNMP_binding.		
DR	InterPro: IPR0016223; K+channel_pore.		
DR	InterPro: IPR000636; M+channel_mlg.		
DR	InterPro: IPR001610; PAC.		
DR	InterPro: IPR000700; PAS_assoc.C.		
DR	InterPro: IPR000014; PAS_domain.		
DR	Pfam: PF00027; CNMP_binding.1.		
DR	Pfam: PF00520; ion_trans.1.		
DR	Pfam: PF00785; PAC.1.		
DR	SMART; SM00100; CNMP.1.		
DR	SMART; SM00086; PAC.1.		
DR	SMART; SM00091; PAS.1.		
DR	TIGRFAMS; TIGR00229; sensory_box.1.		
DR	PROSITE; PSS0042; CNMP_BINDING_3; 1.		
DR	SEQUENCE 1311 AA; 14467 MW; A766C460B833329B CRC64;		

[illegible]

OY	820	CTTGACATTTGGTGAATTTTCCGTACCAATTCGATCCAGATTCGGGACAGTGGTGT	879
OY	880	GCSSCAAGTCCATTTGGCCCACTACGTCACACACCTGGTCTCCCTGATGATCCGA	939
Db	338	ValAspIleuLeuIasnPhenArgIThrPheValSerArgLysGlyValValSer	357
Db	358	AsnSerLysGlnIleAlaIleAsnTyrIleuArgGlyTyrPheAlaLeuAspLeuLeuAla	377
OY	940	CGCGTGGCCCTTTGACCTGTTACTACGCTTCAMAGTCAAGTCATGTTACTGGG	990
Db	378	AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyAsnSer	395
OY	991	---GCCATCTGCTGAAGACGGTGGCCCTGGCCGCTGCTGGCTGGCTGGCTGGCGGGTG	1047
Db	396	HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuLeuLysIle	415
OY	1048	GACCGGATCCGGAGTGCACGCGCGGAGTGGCTACACTGTCATGAGCCGCTGTCGCCCTG	1107
Db	416	AspArgTyrSerGlnHisThrAlaMetIleLeuThrIleuLeuMetPheSerPheThrIleu	435
OY	1108	CTCCGGCACTGGGTGGCTGGCTGGTGGTTTACATTTGCCACGCGGAGATGAGACAGC	1167
Db	436	AlaIleHisThrLeuAlaLysIleTyrPyrValIleAlaValLysGlyLysTyrGlu-----	453
OY	1168	GAATCCAGACTGCTGAG-----ATTGGCTGGCTCCAGAGACTGGCCCGCCGACTGGAG	1221
Db	454	-----TrpPheProGlnSerAsnIleGlyTyrPheGlnIleuLeuAlaLysTyr-----	469
OY	1222	ACTGCCATACACTGGTGGGCGGAGGCGCAGTGGAGGAGAACAGCTCGCGCCAGAGTAC	1281
Db	469	-----	469
OY	1282	AACTCAGACAGCAGCAGCGAGGCCAACGGGAGGGCTGAGCTGCTGGCGGCCCTGC	1341
Db	470	-----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu-----	481
OY	1342	CTCGGCAAGCCCTTACATCACTCCCTCTACTTGGCACTAGACAGCCCTCAACAGCCTGGGC	1401
Db	482	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerIleuThrValGly	498
OY	1402	TTTCGGCAACGTCGGCGCAACAGCGACAGAGAAAGTCTTCCTCCATCTGCACATGTC	1461
Db	499	PheGlyAsnValSerAlaAsnThrThrAlaGlyValAlaPheThrIleIleMetIleLeu	518
OY	1462	ATCGGCGCCCTGATGACAGCGGCTGGTGGTGGAGAGCTGACGGCCATCATCCAGCGCATG	1521
Db	519	IleGlyAlaLeuMetHisAlaValAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMet	538
OY	1522	TACGCGCGCCGCTTCTGTACACAGCCGCAACGCGGACCTGGCGGCATCATCCGCAATC	1581
Db	539	TyrSerArgArgSerLeuTyrGlnSerLysTyrPArgSerPheLysAspPheValAlaLeu	558
OY	1582	CACCGTATCCCAAGCCGCTCAACAGCGAGATGGAGTCCAGACTCCAGGCAACCTGGGG	1641
Db	559	HisAsnMetProLysGlnLeuLysGlnArgIleGlyAspTyrPheGlnThrSerTyrSer	578
OY	1642	GTGACATATGCAATCGACACACACAGCAAGCTGTGAGAGCCCTCCCTGACAGACTCGCGCA	1701
Db	579	LeuSerHisGlyIleAspIleTyrGlnThrLeuArgGlyIlePheProGlnIleuLeuArgGly	598
OY	1702	GACATCGCCATGACACTGTCACAGAGAGCTCTGCAGCTGCCACTGTTTGAAGCGCCAGC	1761
Db	599	AspArgSerMetHisLeuHisArgGlnIleLeuGlnIleuProIlePheGlnAlaAlaSer	618
OY	1762	CGCGGCTCCCTGGGAGCACTCTCTGCGCCCTGGGCGCCGCTTCGACGCGCGGCGAG	1821
Db	619	GlnGlyLysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu	638
OY	1822	TACGTCATCCCAAGGAGGAGGAGCCCTGACGAGCCCTTACTTGTCTGCTGGCTGCATG	1881
Db	639	TyrIleuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysAsnGlySerMet	658

D	40	AlaVal111eTTCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal	59
Q	181	ATGCAGCGGGGCTGTGCTTCCTCCCTTATGGCGACAGACACAGTGTGCTGGC	241
D	60	MetGlnArgProCysThrCysAspPheLeuHisGlyProAlaGlyThrGlnArgAlaAla	79
Q	241	CAACGATCCGCAGAGCCCTGGACGAGACACAAGAGTTCAAGGCTGAGCTGATCTTAC	301
D	80	AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr	99
Q	301	CGGAAGACGGGGCTCCCTTGTGTCTCGATGTGATACCCATGAAGATGAGAA	361
D	100	ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp	111
Q	361	GGGAGAGTGGCTCTCTTCCCTA-----GTCTCTCACAGGACATC-----	391
D	120	GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly	131
Q	400	-----AGCGAAGACAGACAGACGAGGGGGCCCGACATGGAGACAGACAGCT---	441
D	140	SerProThrHisAspThrAsnHisArgGlyProProThrSerTyrPheAlaAlaProGlyArg	151
Q	447	-----	447
D	160	AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrThrArgGluSerSer	171
Q	447	-----	447
D	180	AlaArgProGlyGlyValGlySerAlaGlyAlaProGlyAlaValAlaValAspValAsp	191
Q	447	-----	447
D	200	LeuSerProAlaValProSerArgGluSerLeuAlaLeuAspGluValThrAlaMetAsp	211
Q	447	-----	447
D	220	AsnHisValAlaGlyLeuGlyProMetGluGluGlnArgAlaLeuValGlySerSerSer	231
Q	447	-----	447
D	240	ProProAlaGlyAlaProGluProLeuProSerProAlaGlnHisSerLeuAsnProAsp	251
Q	448	-----GGTGGCGCGCGCGATATGCGCGGACAGATCCAAAGGCTTCATGCCAACCGG	501
D	260	AlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSerVal	271
Q	502	CGGCGG-----	507
D	280	ArgArgAlaSerSerAlaAspAspIleGluIleMetArgAlaGlyLeuProProProPro	291
Q	508	-----ACCGGGCGCGCTCTTACCACCTGTCCGGGCGACCTGCAGAAACGAG-----	551
D	300	ArgHisAlaSerThrGlyAlaMetHisProLeuArgGlyGlyLeuLeuAsnSerThrSer	311
Q	552	-----	552
D	320	AspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeuAsnPhe	331
Q	552	-----	552
D	340	ValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIleIleAla	351
Q	553	CCCAAGGCGACACCAAGCTCATATAGGGGGTGTGGGAGAAACCAAC-----	603
D	360	ProLysIleLysGluArgThrHisAsn-----ValThrGluLysValThrGlnValLeu	371
Q	604	-----TTTGCTGAGTACAAAGTAAAGTACCGCCATCCGGAAGTGGCCCTTC	645
D	378	SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgGlyIleHisArgTyr	397
Q	646	ATGCTGTGGACGTGTGGGCGACGAGGCCACCTGGGATGGCTTCATCTGCTGCCACA	705
D	398	ThrIleLeuHisTyrSerProPheLysAlaValATTTAspThrProLeuLeuLeuVal	417





Db 1067 GlnArgMetThrLeuIleProProAlaValThrPro----- 1083  
QY 2767 GGAGAGGGCGCGCCGACGACACCGCGCTTGCAGCGCTGTGTGGACACT 2826  
Db 1084 -----GlyProGlyProThrSerSerLeuProValSerProIleProThr 1101  
QY 2827 GGGGCGATCCTCTACTGCTGCTGAG-----CCCCCA 2856  
Db 1102 LeuThrLeuAspSerLeuSerGlnValSerGlnPheMetAlaPheGluLeuProPro 1121  
QY 2857 GCTGGCTGTGTGAGTGGAGGACTGGCCGACCGCTGCGGGGCGCTCT---CCCGTC 2913  
Db 1122 GlyAlaProGluLeu-----ProGlnAspGlyProProArgArgLeu 1135  
QY 2914 ATGGCACCCTGGCGCGCTGGGCTGCCGACCGCTGCTGAG 2949  
Db 1136 SerLeuProGlyGlnLeuGlyAlaLeuThrSerGln 1147

## RESULT 12

035221 PRELIMINARY; PRT; 1162 AA.  
AC 035221;  
DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE MERGIA (MERGIA).  
GN KCNH2 OR MERG1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10950;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SV129;  
RX MEDLINE=98012815; PubMed=9351462;  
RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,  
RA Gilbert D.J., Jenkins N.A., Saitler C.A., Robertson G.A.;  
RT "Two isoforms of the mouse ether-a-go-go-related gene coassemble to  
RT form channels with properties similar to the rapidly activating  
RT component of the cardiac delayed rectifier K<sup>+</sup> current."  
RL Cite. Res. 81:870-878(1997).  
DR EMBL; AF012871; AAC53420.1;  
DR EMBL; AF012870; AAC53420.1; JOINED.  
DR EMBL; AF012871; AAC53422.1;  
DR EMBL; AF012870; AAC53422.1; JOINED.  
DR MGD; MGI:1341722; Kcnh2.  
DR InterPro: IPR000595; CNMP\_binding.  
DR InterPro: IPR003967; Erg\_channel.  
DR InterPro: IPR001622; K<sup>+</sup>channel\_pore.  
DR InterPro: IPR000636; M<sup>+</sup>channel\_nlg.  
DR InterPro: IPR001610; PAC.  
DR InterPro: IPR000700; PAS-assoc\_C.  
DR InterPro: IPR000014; PAS\_domain.  
DR Pfam; PF00027; CNMP\_binding.1.  
DR Pfam; PF00520; Ion\_trans.1.  
DR Pfam; PF00785; PAC.1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; CNMP.1.  
DR SMART; SM00086; PAC.1.  
DR SMART; SM00091; PAS.1.  
DR PROSITE; PS00042; CNMP\_BINDING\_3.1.  
SQ SEQUENCE 1162 AA; 126885 MW; A9455F7F10B61E46 CRC64;

## Alignment Scores:

Pred. No.: 5,256-78 Length: 1162  
Score: 1547.00 Matches: 413  
Percent Similarity: 44.21% Conservative: 144  
Best Local Similarity: 32.78% Mismatches: 352  
Query Match: 25,41% Indels: 351  
DB: 11 Gaps: 31

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x 035221 (1-1162)

QY 1 ATCCGCCAGCCGGGGCCCTCTGCGCCCTCAGAACACCTCTGACACATCCGTACG 60  
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20  
QY 61 CGCTTCGACGAGGACGACACAGTACTTCTGCTGGCCAGCCGACGAGGCGGCTCTTC 120  
Db 21 LysPheGlnGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnGly 39  
QY 121 CCGGAGTCTACTGCTGATGAGGCTTCTGACCTCAGCGGCTTCCCGGCTGAGTC 180  
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59  
QY 181 ATGCAGCGGGGCTGCTGCTCTCTCTCTCTTATGGCCGACACACAGTGGAGTCTCCGC 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79  
QY 241 CACAGATCCGCAAGCCCTGGAGCAGCACAAGATTCAGAGCTGATCTGTATC 300  
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
QY 301 CGAAGAGCGGGCTCCCGTGTGCTGCTGATGATGATACCATTAAGATGAGAA 360  
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119  
QY 361 GGGAGGTGGCTCTCTCTCTA-----GTCTTCACAGGACATC----- 399  
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValAlaMetGluLysAspMetValGly 139  
QY 400 -----ACGAAACCAAGACCGAGGGGCCCGCCGACATGAGACAGAGT--- 447  
Db 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTyrLeuAlaSerGlyArg 159  
QY 447 ----- 447  
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuAlaLeuThrAlaArgGluSerSer 179  
QY 447 ----- 447  
Db 180 ValArgThrGlySerMetHisSerAlaGlyAlaProGlyAlaValAlaValAspValAsp 199  
QY 447 ----- 447  
Db 200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219  
QY 447 ----- 447  
Db 220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlySer 239  
QY 447 ----- 447  
Db 240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259  
QY 448 -----GGTGGCGCGCGCGCATATGCGCGGACAGATCCAAAGGCTTCATATGCC 495  
Db 260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279  
QY 496 AACCGGCGCGGAGCGCGGCC-----GTGCTTACACCTGTCGGGCGACCTGACG 546  
Db 280 SerValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyAlaLeuPro 299  
QY 547 AACGAGCCCAAG-----GGCAACACACAGTCAATTAAGGGGCTTTGGG 591  
Db 300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319  
QY 592 GAGAAACCAAC----- 603  
Db 320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339  
QY 603 ----- 603  
Db 340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359

QY	603	-----	603
Db	360	llellealprolysillelysglnlgrthrhlnhsanvaltlrhglulysvaltlrhglnval	379
QY	604	-----TTGGCTGAGTCAAAAGTACGCCCATCGGAAGTCGGCC	642
Db	380	leuserleuglyalaspvalleuprogulutrllysleuglnalalalprokarglilenlsatg	399
QY	643	TTCACTCTGTTCACATGTGTGGGCGACTGAGAACCCACTGGGATGGCTTCACTGCTCGCC	702
Db	400	tlrhlrllelelnhlslyserprophelysalavaltrapsrlpreulleuleuleu	419
QY	703	ACACTATGTGTCTGTCTACTGTGCGCTTACAGCGTGTGTGTC-----	744
Db	420	valtlelythralavalphethrlprotyrserlalaalalpheuleuleulysglutrhgln	439
QY	745	-----AGACACGACGAGGAGGCCAGTGGCGCGCGCGCGCGCGCGCGCGCTGTGACAGT	798
Db	440	asrglyserglnalalprospcysglutryalacysglnproleulavalvalaspheu	459
QY	799	GCGCGGAGGCTGCTCTTCATCCCTTCATCTGACATGTGCTGATATTCGCTGACATTCGCTG	858
Db	460	llevalasprllelnerhellavalasprlleleulaleasnphemrghthrlthryvalasn	479
QY	859	AAATCGGCGAGAGTGGTGTGTGGCCCAAAAGTCATTTGGCTCCACTACAGTCACACACTGG	918
Db	480	alasnrglnlvalvalserhlnsprogulagllalvalahlslyrheulysglutyr	499
QY	919	TTCTCTGATGTCTCATCGACGGCTGCGCTTTCAGCTGTGATCGCTTCAAGTGCAC	978
Db	500	phelenuleasprethvalaalalaleprophelaspreu-----	513
QY	979	GTGTACTTGGGGCC-----CACTGTGAAGAGTGCGGCTGTGCTG	1020
Db	514	---llephedylserlysergluglnleulleglyleuulyslthralaalgrleu	532
QY	1021	CGGCTGTGGCGGCTGTGCTCGGCGGCTGGAGCGGACTCGGATACAGCGCGGTGTGCTG	1080
Db	533	argleuvalatrgalalalarglylsleuasparglyrserltutryglalalavalleu	552
QY	1081	ACACTCTCATGGCCGCTGTGTGCGGCTGACCTGGGCGACTGGGTGCGCTGCTGTGTTTAC	1140
Db	553	phleuleuleutylsyrhrhealaleullelnhlsrlpheulacyslietrlptylala	572
QY	1141	ATTGGCCAGCGGAGATCGAGACAGCGAATCGAGTGTGCTGATGTGCTGGCTGCAG	1200
Db	573	lleglyasmetgluglnprohlsmetlaser-----Hslleglytrpleuhls	589
QY	1201	GACGTGCGCCGCGGACTGAGACTCCCTTACTACCTGTGGGCGGAGGCCAGCTGGAGGG	1260
Db	590	Asnleuglyasprlnlleglyllysprotyr-----	599
QY	1261	AACAGTCCGGCCAGAGTAGACAACTGTGAGAGAGAGAGAGGCGCAAGCGGGGCTG	1320
Db	600	Asnserlserly-----	603
QY	1321	GACCTGTGGGCGCGGCTGTGCGGCGAGCGGCTACATCACTGCTTACTTGGCACTG	1380
Db	604	-----leuylglyproserllelysasprlytyrvaltlhralaleutyrphethrph	621
QY	1381	AGCAGCTCACAGCGTGGCTTCGCGAGCGTGTCCGCGACAGCGACCGAGAGATC	1440
Db	622	SerSerleuthrservalglrphleglyasnvalserproasntrhansserglulyslle	641
QY	1441	TTCTCATGTGCACCATGCTCATGTGGCGGCTGTATGCAGCGGCTGTGTGGAGAGTG	1500
Db	642	Pheserllecyvalmetleullelleglyserleuemetrylaserllephleglyasnval	661
QY	1501	ACGGCATCATCACAGCGATGACGCCGCGCTTCTGTACACAGCGCGACCGCGGAC	1560
Db	662	Serlallellelgnatrgleutyrserglythralaalrglyrhlnstlghlnmetleuarg	681
QY	1561	CTGGCGACATACATCCCGCATTCACACCGATATCCCAAGCGCCCTCAAGAGCGCATGTGGAG	1620

Db	682	ValArgGluPheLeuPheArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGlu	701
QY	1621	TACTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCCAGGACCTGGTCGACAG	1680
Db	702	TyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly	721
QY	1681	CTCCCTGACAGGTGGCGGCGAGACATGGCCAGTCGACACGCAAGGAGGCTGTCCAC	1737
Db	722	PheProGluLysLeuGlnAlaAspIleCysLeuHisIleAsnArgSerLeuGlnHis	741
QY	1738	CTGGCATCGTTTGAGCGGCGACCCGCGGCTCTCGCGGACACTGTCTGGCCCTTCGG	1797
Db	742	CysLysProPheArgGlyAlaThrLysGlyCysLeuAlaGlyAlaLeuAlaMetLysPheLys	761
QY	1798	CCCGCTTTCGACAGCCGCGGCGAGTACCTCATCCACCAAGCGATGCCCTGACGGCCTC	1857
Db	762	ThrThrHisAlaProProGluAspThrLeuValHisAlaGlyAspLeuThrAlaLeu	781
QY	1858	TACTTTGTCTGTGGCTTCGATGAGAGGTGTCAAGGTTGGACCGCTGTCCGATCTTA	1917
Db	782	TyrPheIleSerArgLysSerIleGlnIleLeuAlaGlyAspValAlaValAlaIleLeu	801
QY	1918	GGGAAGGGCCACCTGATGGCTGTGAGCTGGCCCGCGGAGACAGCTGTAAAGCCAA	1977
Db	802	GlyLysAsnAspIlePheGlyLeuProLeuAsnLeuTyrAlaArgProGlyLysSerAsn	821
QY	1978	GCGCAGTGAAGGGCGGACGTACTGATCGATCGATGCTGACGTGGCTGGCTGCAC	2037
Db	822	GlyAspValAlaGlyAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspLeuLeu	841
QY	2038	GACAGCCTTGGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCTGGCTCCGAGGGAG	2097
Db	842	GluValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu	859
QY	2098	CTCAGTACACCTG-----GGTCTGGGGAGGCTCTGCAGAGCT	2139
Db	860	IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeu	879
QY	2140	GACACCACTCCCTGACGGCGACGACATACCCTTAATGTCCACGCTGGAGAGAAAGAGCA	2199
Db	880	GluSerGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLys	899
QY	2200	GATGGGAGACGGGCGCCAGCGTCCCGACGCCGACGTGATGAGACCTCCAGCCCTCG	2259
Db	900	AspIhrGluGln-----	903
QY	2260	CTGTCCCTGGCTGACACTCTCATCTCCAGTGCACAGCTGTATCCCGACGTGACAA	2319
Db	904	-----ProGlyGluValSerAlaLeuGlyGln-----GlyProAlaArgVal	917
QY	2320	GCACCCCGGCTCTGTAGGTGGCAGAGGAGGCCAGGAGGCGAGGGCTTTGAAGGCT	2379
Db	918	GlyProGlyLysProSerCys-----ArgGlyGlnProGlyGlyProThrGlyLysSerPro	935
QY	2380	GAGCTGGCCCCCTGCTCCCCA-----CGGGCCCTTAAG	2415
Db	936	SerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSer	955
QY	2416	GGGCTACGGGCTCCCCCATGCCATGGAATGTGCCCCCAGATGTGAGCCCCAGGGTACTA	2475
Db	956	ProLeuArgLeuValProPheSerSerProArgProProGlyLysProProGlyGlyGlu	975
QY	2476	GATGGCATTGAAGAGGGGTGGCTGGCAGCACGCCAAG-----	2514
Db	976	ProLeuThrGluAspGlyGlyLysSerAspThrCysAsnProLeuSerGlyAlaPheSer	995
QY	2515	-----TTCTCTTTT-----CGCGTGGCGCAGTCTGGC	2541
Db	996	GlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnIhrGlnGluLeu	1015
QY	2542	CGGAGTGTAGCAGACGCCCTCCCTGACCAAGAGAGGGGCTGTCTCACTTTCC---	2598

Pred. No.:	8 756-78	Length:	1162
Score:	1563.00	Matches:	416
Percent Similarity:	44.25%	Conservative:	142
Best Local Similarity:	32.99%	Mismatches:	350
Query Match:	25.34%	Indels:	33
DB:	6	Gaps:	33

  

US-09-965-830-1_COPY_6_3257 (1-3252) x Q8WNY2 (1-1162)	
QY 1 ATGCGGCGCATGGGGGCGCTCCGGGCGCTCGAACACCTTCCTGGACACCTTCGACACCTTCGAC	60
DB 1 MetcProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspPrfThrIleLeArg	200
QY 61 CGCTTCGACGGCAGCAGACAGTAACTTCGTGGTGGGAGCAGCGCCAGTGGGGGGGCTCTTC	120
DB 21 LysPheGluLysLysSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys---	39
QY 121 CCGGTGCTACCTGCTCTGTATGGCTTGTGTGACCTCAGCGGCTTCTCCCGGCTGAGTGC	180
DB 40 AlaValIleArgTyrAsnAspArgLysPheCysGluLeuCysGlyTyrSerArgAlaGluVal	59
QY 181 ATGAGCGGGGCGTCCCGCTCTCTCTTATGGCGGACAGACACCACTAGCTGCTCCG	240
DB 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla	79
QY 241 CAACAGATCCGCGAAGCGCCCTGAGCAGACAGACAGTCAAGCGTGAAGCTGATCCCTGAC	300
DB 80 AlaGlnIleAlaGlnAlaLeuLeuGluValAlaGluGlnArgLysValGluIleAlaPheTyr	99
QY 301 CGGAGAGCGGGGCTCCCTGTGTGTCTCTGCTGATGTATACCAATGAAGATGAGAA	360
DB 100 ArgLysAspArgLysCysPheLeuCysLeuValGlyValAlaProValLysAsnGluAsp	11
QY 361 GGGGAGTGGCTCTCTC-----CTAGTCTCTGACAGACATC-----	39
DB 120 GAlaValAlaIleMetPheValLeuAsnPheGluValAlaValMetGluLysAspMetValGly	13
QY 400 -----AGCAACAGCAGACGAGGGGGCGCCCGCCAGATGAGACAGACAGT---	44
DB 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerThrPheLeuAsnSerGlyArg	15
QY 447 -----	44
DB 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgLysSer	17
QY 448 -----GGTGGCGGGCGCCGATATGCG-----	46
DB 180 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaValValAlaAspAlaAsp	19
QY 468 -----	46
DB 200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGlyValSerAlaMetAsp	21
QY 468 -----	46
DB 220 AsnHisValAlaGlyLeuGlyProAlaGluGlnArgAlaGluValGlyProGlySer	23
QY 468 -----	46
DB 240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn	25
QY 469 -----CGGGCAGATCCCAAGCGCTTATATGCC	49
DB 260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGlnSerCysAla	27
QY 496 AAGCGGCGCGGAGCGCGGCG-----GTGCTTACCACTTCCCGGCGACCTGCAG	54
DB 280 SerValArgAlaGlyAlaSerSerAlaAspArgIleGluAlaMetArgAlaGlyAlaLeuPro	29
QY 547 AAGCAGCCCAAG-----GGCAGCAGCAGCTCATTAAGGGGGGCTTTGGG	59
DB 300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn	31

592 GAGAACCAAC----- 603  
320 SerHisSerAspSerAlaValArgTyrArgThrIleSerLysIleProGlnIleThr 339  
603 ----- 603  
340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359  
603 ----- 603  
360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrGluValThrGlnVal 379  
604 ----- 642  
380 LeuSerIleGluAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArg 399  
643 TTCACCTGTTGACACTGGGGGACACTGAGACCCACCTGGAGTGCCTGACCTGGCC 702  
400 TrpThrIleLeuHisLysSerProPheLysAlaValTrpAspTrpLeuIleLeuLeu 419  
703 ACACCTATGCGCGCTGACAGTGGCTACAGCGCTGCTGCTG----- 744  
420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 439  
745 -----AGCACAGCAGGAGCGCCAGTCCGCGCGCGCGCGCGCGCGCTGTGACCTG 798  
440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspLeu 459  
799 GCGGTGAGGCTCTGCTGATCCTGACATGTGCTGATTTCCGATCCACATCTGCTGCC 858  
460 IleValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsn 479  
859 AAGTCGGGCGCAGGTGTGTTTCCCAAGTCCATTTGCTGCTGACCTGACCTGACCTG 918  
480 AlaAsnGluGlnValValSerHisProGlyArgTyrIleAlaValHisLysThrLysGlyTyr 499  
919 TTCCTGCTGATGATGATGACGAGCGCTTGCACCTGCTGACCTGCTGACCTGCTGAC 978  
500 PheLeuIleAspMetValAlaAlaIleProPheAspLeu----- 513  
979 GTGTACTTGGGGGCT-----CATGCTGTAAGACGGTGGCGCTGCTG 1020  
514 -----IlePheGlySerLysGluGluIleGlyLeuLeuLysThrAlaArgLeuLeu 532  
1021 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
533 ArgLeuValArgAlaAlaArgLysLeuAspArgTyrSerGlyTyrGlyAlaValAla 552  
1081 ACACCTGCTATGCGCTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
553 PheLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleIleTyrAla 572  
1141 ATTTGGCCACGGAGATCGAGACGACGACGACGACGACGACGACGACGACGACGACGAC 1200  
573 IleGlyAsnMetGlnProHisMetAspSer-----HisIleGlyTrpLeuHis 589  
1201 GACCTGCGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1260  
590 AsnLeuGlyAspGlnIleGlyLysProTyr----- 599  
1261 AACAGCTCCGCGCAGAGTGAACATCGACGACGACGACGACGACGACGACGACGACGAC 1320  
600 AsnSerSerLys----- 603  
1321 GACCTGCTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
604 -----LeuIleGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPhe 621  
1381 AGACGCTCACACGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
622 SerSerLeuThrSerValIleGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle 641  
1441 TTCTCCATCTGCACACATGCTCATGCGCGCGCTGATGACGCGGTGGTGTGGAGACGTG 1500

642 PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal 661  
1501 ACGGCATCATCCACGCGATGATAGCCCGCGCTTCTGTGATCCACGCGGACGCGGAC 1560  
662 SerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg 681  
1561 CTGGCGCACTACATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGAT 1620  
682 ValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlu 701  
1621 TACTTCCAGCGCCACTGGGCGGTGAAACAATGGCATCGACACACCGACCTGCTGAGAC 1680  
702 TyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly 721  
1681 CTCCCTGACGACCTGCGCGCAGACATCGGCATGCACTGCGACAGAGAGCTCTGAC---- 1737  
722 PheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHis 741  
1738 CTGCCACTGTTTGAGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1797  
742 CysLysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLys 761  
1798 CCGGCGCTTGTGACCGCGCGCGAGTACCTCATCCACCAAGCGCATGCTGCGACGCGCTC 1857  
762 ThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeu 781  
1858 TACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1917  
782 TyrPheIleSerArgLysIleGluIleLeuArgGlyAspValValThrAlaIleLeu 801  
1918 GGGAAAGCGCACTGATCGCTGTGAGCTGCCCGCGCGGAGCAGAGTGTAAAGCCAT 1977  
802 GlyLysAsnAspIlePheGlyLeuProLeuAsnLeuTyrAlaArgProGlyLysSerAsn 821  
1978 GCGGACGTAGAGGGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037  
822 GlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeu 841  
2038 GACAGCTCGCGCTGACCGCGAGTGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 2097  
842 GluValLeuAspMetTyrProGluPheSerAspHisPheThrSerLeu-----Glu 859  
2098 CTCAGCTACACCTG-----GGTGTGGGGGAGCTCTGCGAGAGGTG 2139  
860 IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeu 879  
2140 GACACCACTCCCTGAGCGCGCAGCAATACCTTATGTCACGCTGAGAGGAAGAGACA 2199  
880 GluSerGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgThrAspLys 899  
2200 GATGGGAGCAGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2259  
900 AspThrGluGlnProGlyGluVal-----ProAla 909  
2260 CTGTCCCTGCTGCGACCTCCTCATCTGACGTCGCAAGCTGATCCGACGCTGACACA 2319  
910 LeuGlyGlnGly-----ProAlaArgVal 917  
2320 GCAACCGCGCGCTGCTGAGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2379  
918 GlyProGlyProSerCys-----ArgGlyGlnProGlyArgProThrProGlyLysPro 935  
2380 GAGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2415  
936 SerSerLysProSerSerProGluSerSerGlnAspGlyProGlyArgSerSerSer 955  
2416 GGGCTACGCTGCG 2475  
956 ProLeuArgLeuValProPheSerSerProArgProProGlyAspProProGlyGlyLeu 975  
2476 GATGCAATTGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2514

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Db 976 ProLeuThrGluAspGlyLeuLysSerAspThrCysAsnProLeuSerGlyAlaPheSer 995
QY 2515 -----TTCTCTTC-----CGCGTGGCCAGTCTGGC 2541
Db 996 GlyValSerAsnIlePheSerPheThrPglYAspSerArgGlyArgGlnInrGlnGluLeu 1015
QY 2542 CCGGAATGAGCAGCAGCCCTCCCTGGACGAGAGAGGGCGCTGCTCACTGTTCC-- 2598
Db 1016 ProArgCys-----ProAlaProIleProSerLeuLeuAsnIleProLeu 1030
QY 2599 -----CATGGCCCGCAGCAGGCAAGACACAGACACTGGAC 2637
Db 1031 SerSerProGlyArgArgSerArgGlyAspValGluSerArg-----LeuAsp 1046
QY 2638 AGCTTCGGCAGCGGTGACAGAGCTGACAGACAGTGTG--CTGCAGATCGGGAAAGCA 2694
Db 1047 AlaLeuGlnArgGlnLeuAsnArgLeuGluProArgLeuSerAlaAspMetAlaThrVal 1066
QY 2695 CTGCAGTCACTTCGCCAGCTGTGACCTTGCTGGCGCCACAGAGAGGTCCGTGC 2754
Db 1067 LeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1076
QY 2755 CCTCGGCGATCGGAGAGGGGCGCTGCCAGCAGCAGCTCCGCGCTTCAGACCTTCG 2814
Db 1077 -----ValProAlaIleSerAla----- 1083
QY 2815 TGTGTGACACTGGGGCATCTCTCTACCTGCGTCAGCCCCAGCTGCTGTCTGACT 2874
Db 1084 -ValThrThrProGlyProGlyProThrSerAlaSerProLeuLeuPro-----Va 1100
QY 2875 GGGACTGGCCCCACCTCGTCCGGGCGCTCTCTCCCTCATGACACCTGGCGCTGGGT 2934
Db 1100 LglYProValProThrLeuThrLeuAspSerLeuSerGln-----Va 1114
QY 2935 CCCCCCGCGCTC-----AGAGCTCCCGCTCGCTGACACAGCTTTCTGGAC 2985
Db 1114 LserGlnPheValAlaPheGlyGluLeuProAlaGly---AlaProGluLeuProGlnAs 1133
QY 2986 TCCACCTAGACTAGAGAGCCCTGCTGCTGAGAGACCTGCTGTGAGCCAGACCCCT 3045
Db 1133 pglYProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaPheThrSerGlnProLe 1153
QY 3046 G 3046
Db 1153 u 1153
RESULT 14
035219 PRELIMINARY; PRT; 1162 AA:
ID 035219;
AC 035219;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Ecther-a-90-90-related protein Isoform Mergla.
GN CNH2 OR Merg1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RX MEDLINE=98012815; PubMed=9351462;
RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Sattler C.A., Robertson G.A.;
RT "Two isoforms of the mouse ether-a-90-90-related gene cosegregate to
RT form channels with properties similar to the rapidly activating
RT component of the cardiac delayed rectifier K+ current."
RL CIRC. Res. 81:870-878(1997).
DR EMBL; AF012868; AAC53418.1;
DR MGD; MGI:1341722; Kcnh2.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR003967; Erg_channel.

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DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc.C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00277; CNMP_binding.
DR Pfam; PF00520; Ion_trans.1.
DR Pfam; PF00785; PAC.1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; CNMP.1.
DR SMART; SM00086; PAC.1.
DR SMART; SM00091; PAS.1.
DR PROSITE; PS00042; CNMP_BINDING_3; 1.
SQ SEQUENCE 1162 AA; 126993 MW; B5B16D5FDA3DA81 CRC64;

Alignment Scores:
Score: 1.46e-77 Length: 1162
Percent Similarity: 1539.00 Matches: 414
Best Local Similarity: 44.298 Conservative: 144
Query Match: 32.868 Mismatches: 351
DB: Query Match: 25.288 Indels: 351
Gaps: 32

US-09-965-830-1_copy_6_3257 (1-3252) x 035219 (1-1162)
QY 1 ATGCCGGCATTCGGGGGCTCTGCGCCCTCAGAACCTCTCTGGACACCATGCTACG 60
Db 1 MetProValArgArgGlyAsnValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20
QY 61 CGCTGAGGAGGAGCAGCAGTAACTTGTGCTGGGCAAGCCGAGGAGGGGGGCTTTC 120
Db 21 LysPheIleIleGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnGly 39
QY 121 CCGGTGTACTACTCTGTGATGAGCTCTGTGACCTCAGCGGCTTCGCCGGCTGAGTTC 180
Db 40 AlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 59
QY 181 ATGCAGCGGGGCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 60 MetGlnArgProCysThrCysAspPheLeuIleIleIleIleIleIleIleIleIleIle 79
QY 241 CACAGATCCGCAAGCCCTGAGCAGCAGACAGAGTCAAGGTGAGCTGATCTGATC 300
Db 80 AlaGlnIleAlaGlnAlaIleLeuGlyAlaGluIleArgLysValGluIleAlaPheTyr 99
QY 301 CGGAGAGCGGGGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 100 ArgLysAspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 119
QY 361 GGGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
Db 120 GlyAlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 139
QY 400 -----AGCGAAGCAGAACGAGGGGCGCCGACAGATGGAAGACAGAGT-- 447
Db 140 SerProAlaIleAspThrAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsn 159
QY 447 ----- 447
Db 160 AlaIleThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSer 179
QY 448 -----GTGGCGCGCGCCGATAGGC----- 468
Db 180 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaValAlaAspValAsp 199
QY 468 ----- 468
Db 200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219
QY 468 ----- 468
Db 220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlySer 239

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[illegible]

Db	553	PhenLeuMetCysThrPheAlaLeuIleValHisTrpLeuAlaCysIleTrpGlyAla	572
QY	1141	APPGGCGAGGGGCGAGATCGAGAGAGGAGAGCGAGCTGCGATGAGTGGCGCTGAG	1200
Db	573	IleGlyAsnMetGluInProHisMetAspSer-----HisIleGlyTrpLeuHis	589
QY	1201	GAGCTGGCCCGCCACAGTGGAGAGACTGCTTACCTGGTGGCGCGGAGGAGCACTGGAGGG	1260
Db	590	AsnLeuGlyAspGlnIleGlyLysProGly-----	599
QY	1261	AACAGCTCGGCGCGAGTGTGACATGCGAGCGAGAGCGAGCGGCGAGCGGGCTG	1320
Db	600	AsnSerSergly-----	603
QY	1321	GAGCTGCTGGCGCGCGCTGCTGCGAGCGCTACATGACTGCTCTTACCTGGCACTG	1380
Db	604	-----LeuGlyGlyProSerIleLysAspLysValValTrpAlaLeuGlyPheThrPhe	621
QY	1381	AGGAGCGCCACCGAGCGGGCTTCGGACATGTCGCGCAACAGGACCGAGAAAGTC	1440
Db	622	SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGlyLysIle	641
QY	1441	TTTCTCATCTGCACCATGTCATCGCGCGCGCTATGCACTGCGAGTGGTGGTGGAACTG	1500
Db	642	PheSerIleCysValMetLeuIleGlySerLeuMetGlyAlaSerIlePheIleAsnVal	661
QY	1501	ACGGGCATCATCGAGCGGACATGATGCGCGCGCGCTTCTTACACAGCGCGCGCGAC	1560
Db	662	SerAlaIleIleGlnArgLeuGlySerGlyThrAlaArgTyrHisTrpGlnMetLeuArg	681
QY	1561	CTGGCGCATCATCGCGCATCGCATCGCATCGCGCGCGCTGCGAGCGCATGCTGGAG	1620
Db	682	ValArgGlyPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnIu	701
QY	1621	TACTTCAGAGCGCACTGGGGGGGGTGAACATGGATGGATGAGAACACCGAGCTGGAGAC	1680
Db	702	TyrPheGlnHisAlaIleArgSerTyrThrAsnGlyIleAspMetAsnAlaValIleLysGly	721
QY	1681	CTCCCTGACGAGCGCGCGGAGACATCGGCATCGCATCGCTGACAAAGAGCTCGTGCAG---	1737
Db	722	PheProGluCysValLeuGlnAlaAspIleCysValLeuHisLeuAsnArgSerLeuLeuGlnHis	741
QY	1738	CTGGCATGTTTGAGGGCGGCGAGCGCGCGGCTGCTGCGGGCATCTGCTGGCGCTGGG	1797
Db	742	CysLysProPheArgGlyAlaIleTrpLysGlyCysLeuAlaArgAlaLeuAlaMetLysPheLys	761
QY	1798	CCCGCTCTTGTGACGCGCGGGCGAGTCACTATCGACCAAGGAGATCGCTGCGAGGCTG	1857
Db	762	ThrTrpHisAlaProProGlyAspTrpIleValHisAlaGlyAspLeuIleThrAlaLeu	781
QY	1858	TACTTTGCTCTGCTGGCTGCTGCATGAGAGTGTCAAGAGTGGACCGCTGCTGGCTGCTG	1917
Db	782	TyrPheIleSerArgGlySerIleGlnIleLeuArgGlyAspValValAlaIleLeu	801
QY	1918	GGGAGGGCGGACATCGCTGCTGAGCTGCGCGCGCGGGGAGACAGTGTAAAGCCAAAT	1977
Db	802	GlyLysAsnAspIlePheGlyGlyProLeuAsnIleTyrAlaArgProGlyLysSerAsn	821
QY	1978	GCGGACGGAAGGGGCGAGCTAGCTGGCTGCTGCACTGCTGAGCTGGCTGGCTGAG	2037
Db	822	GlyAspValArgAlaLeuTrpTyrCysAspLeuHisLysIleHisAlaGlyAspSerLeu	841
QY	2038	GACAGCCCTTGGCGCTGCGCGCGAGTGGTGGCGCGCGCGCTGAGTGTGGCTGCGAGGGAG	2097
Db	842	GluValIleAspMetTyrTrpGluProGluPheSerAspHisPheTrpSerLeu-----Glu	859
QY	2098	CTGACATCAACATG-----GGTGTGGGGGAGCTGTGCAGAGGTG	2139
Db	860	IleThrPheAsnLeuArgAspTrpHisMetIleProGlySerProSerSerAlaGlyLeu	879
QY	2140	GACACAGACTCTGCTGAGCGGCGACAAATTCCTTATGTCACAGCTGGAGAGAAAGAGACA	2199

Db 880 GluSerGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgThrAspLys 899  
QY 2200 GATGGAGGACGAGGAGCCACGGTCTCCACGCCACGATGAGCCCTCCAGCCCTG 2259  
||| |||||  
Db 900 AspThrGlnGln----- 903  
QY 2260 CTGTCCCTGGCTGCACCTCTCATCTCAGTGCACAGCTGTATCCACGTCGACAA 2319  
||||| |||||  
Db 904 -----ProGlyGlnValSerAlaLeuGlyGln-----GlyProAlaArgVal 917  
QY 2320 GCACCCCGGCTCTGCTAGTGGCAGAGGAGGCCAGCAGCGCGAGGCTTGAAGCT 2379  
||| |||  
Db 918 GlyProGlyProSerGys-----ArgGlyGlnProGlyGlyProThrGlyGluSerPro 935  
||||| ::|||  
QY 2380 GAGGCTGGCCCTCTGCTCCCA-----CGGCCCTAGAG 2415  
:::|||||  
Db 936 SerSerGlyProSerSerProGluSerSerGluAspGlyProGlyArgSerSer 955  
:::|||||  
QY 2416 GGGCTAGCGGCTGCCCCCATGATGATGATGATGATGATGATGATGATGATGATGAT 2475  
||||| |||  
Db 956 ProLeuArgLeuValProPheSerSerProArgProGlyAspSerProGlyGlyGlu 975  
||||| |||  
QY 2476 GATGCAATGAGAGCGGCTGGCTGGCCAGACCC----- 2511  
||||| |||  
Db 976 ProLeuThrGluAspGlyGlyLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 995  
||||| |||  
QY 2512 -----AAGTTCTCTTC-----CGCTGGGCCAGTCT 2538  
||||| |||  
Db 996 SerGlyValSerAsnIlePheSerPheThrGlyAspSerArgGlyArgGlnIleGln 1015  
||||| |||  
QY 2539 GGGCCGGAATGTAGCAGACACCCCTCCCTGGACAGAGAGCGGCTGCTACTGTTCC 2598  
||| |||  
Db 1016 LeuProArgGys-----ProAlaProAlaProSerLeuAsnIlePro 1030  
||||| |||  
QY 2599 -----CATGGGCCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2634  
||| |||  
Db 1031 LeuSerSerProGlyArgArgSerArgGlyAspValGlnSerArg-----Leu 1046  
||| |||  
QY 2635 GACAGCTTGGGAGGCGGTGACAGAGCTGTACAGACGAGTG---CTGCAGATGCGGGAA 2691  
||| |||  
Db 1047 AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnThrArgLeuSerAlaAspMetAlaThr 1066  
||| |||  
QY 2692 GGAAGTCACTGCTGCGCAGGCTGTGACGTTGCTGGCGGCCACAGGAGGAGTCCG 2751  
||||| |||  
Db 1067 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1077  
QY 2752 TGGCTTCGGGATCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2811  
||||| |||  
Db 1078 -----ValProProAlaThrSerAla-- 1084  
QY 2812 CTGTGTGTGACACATGGGATCTCTACTGCTGACGCGCCACGCTGGCTGTCTTG 2871  
||| |||  
Db 1085 -----ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuPro----- 1100  
QY 2872 AGTGGACTTGGCCCACTGCTGCGGAGGCTGCTCCCTCATGACACCTGGCCCTGG 2931  
||||| |||  
Db 1101 -ValGlyProValProThrLeuThrLeuAspSerLeuSerGln----- 1114  
QY 2932 GGTCCCCAG-----CGTCTCAGAGCTCCCTGCGCTGAGCCACAGCTTCTGAGCC 2985  
||| |||  
Db 1115 -ValSerGlnPheValAlaPheGlnGlnLeuProAlaGlyAlaProGlnLeuProGlnAs 1134  
QY 2986 TCCACCTCAGACTCAGAGCCCTGCTCAGAGACCTGCTCTGAGCCACGACCCCT 3045  
||| |||  
Db 1134 pGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLe 1154  
QY 3046 G 3046  
Db 1154 u 1154

